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1
A

2 32
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62 92
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122 152
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr

362 392
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 1

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722 752
ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

782 812
TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

842 |Cadherin Cleavage| 872
GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902 932
GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962 992
AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly

1022 1052
TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082 1112
CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142 1172
TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202 1232 |Cadherin EC
GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

xxx| 1292
GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu

1322 1352
AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala

1382 1412/471
AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442 1472
AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser

FIG. 1 (cont.)

1502
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn

1532
1562
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1592
1622
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp

1652
1682
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1712
1742
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1772
1802
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1832
1862
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val

1892
1922
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1952
1982
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2012
2042
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2072
2102
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

2132
2162
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

2192
2222
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

2252

FIG. 1 (cont.)

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2282                                2312
TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342                                2372
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402                                2432
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462                                2492
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522                                2552
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582                                2612
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642                                2672
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702                                2732
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762                                2792
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822                                2852                                |XXXXXXXXXXXXXXXXXXXX Predicted
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

Transmembrane Domain XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX|
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942                                2972
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu

3002                                3032
GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG
asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062                                3092
TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT
cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

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FIG. 1 (cont.)


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3122                                     3155
ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT
ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

3182                                     3212
ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG
ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu

3242                                     3272
TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC
tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

3302                                     3332
CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT
pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3362                                     3392
GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC
asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

3422                                     3452
TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG
phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln

3482                                     3512
TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC
cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys lys arg ile

3542                                     3572 |XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG
pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

3602 xxx Coiled-Coil 1 XXXXXXXXXXXXXXXXXXXX 3632 xxx Coiled-Coil 1 XXXXXXXXXXXXXXXXXXXX
AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA
ser lys lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys

3662 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX| 3692
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3722                                     3752
GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG
ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

3782                                     3812 |XXXXXXXXXXXXXXXXXXXXXXXXXXXX
CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu

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FIG. 1 (cont.)

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3842 xxx Coiled-Coil 2 xxxxxxxxxxxxxxxx 3872 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA
arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

3902 xxx Coiled-Coil 2 xxxxxxxxxxxxxxxx 3932 xxxxxx|
ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022 |xxxxx PBM xxxxxx|
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG
met val his gly met thr ser ser ser ser val val STP

4082
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142
ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262
GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

4442
CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502
GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562
TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT

4622
GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682
TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742
ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802
TTT ACT
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FIG. 1 (cont.)

(Nucleotide position for insertions and deletions are found above the Human (h) CLASP-2A line diagram. Numbers are referenced based on hCLASP-2A nucleotide sequence from Figure 1.)

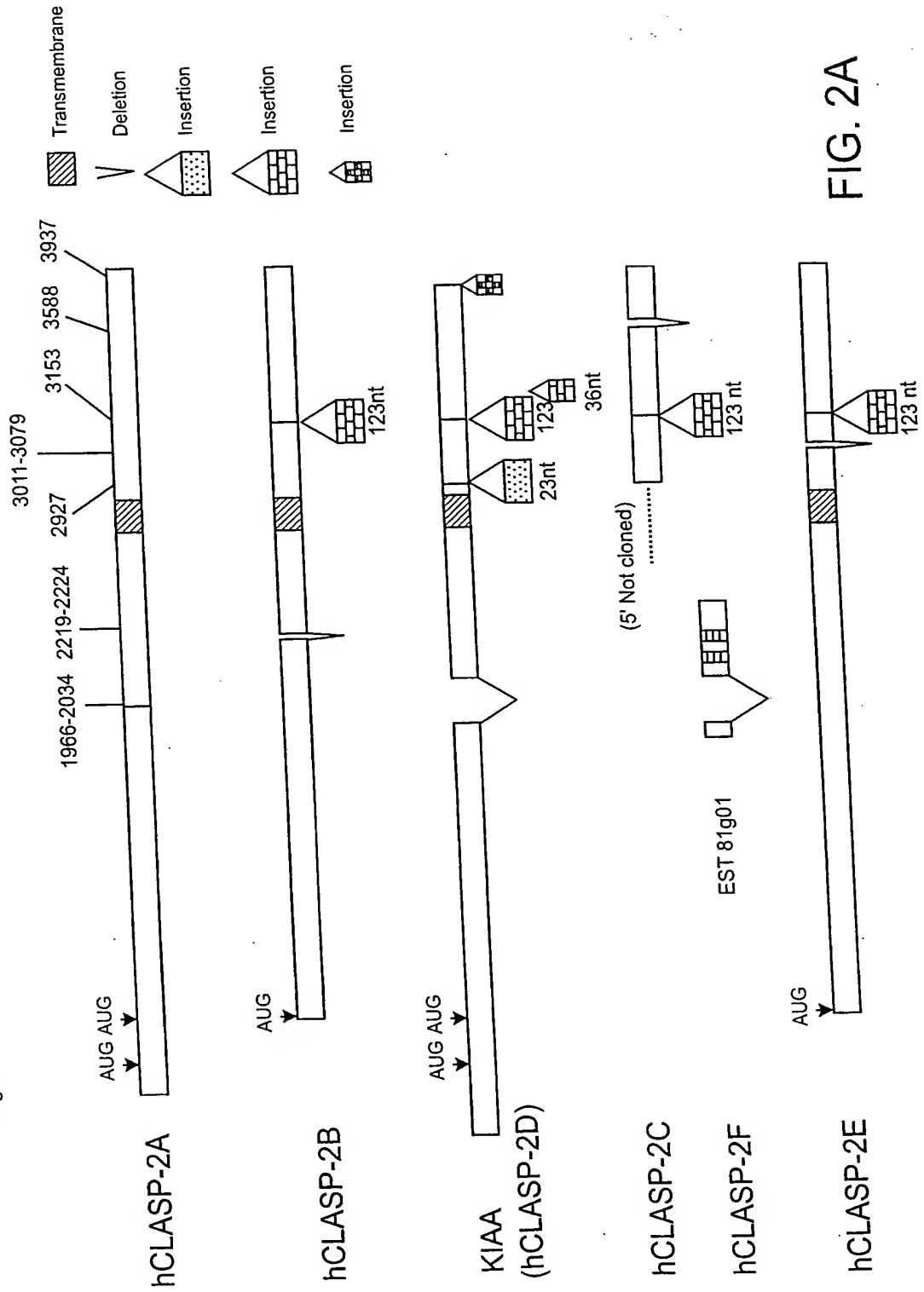


FIG. 2A

2
 GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT
 val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62
 CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA
 gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122
 AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT
 ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182
 CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC
 pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242
 CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA
 leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302
 ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA
 ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr

362
 GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT
 val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422
 GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA
 gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482
 GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC
 gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542
 AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC
 arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602
 CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG
 gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662
 GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG
 ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 2B

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722                               752
ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

782                               812
TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

842                               872
      |Cadherin Cleavage|
GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902                               932
GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962                               992
AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly

1022                               1052
TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082                               1112
CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142                               1172
TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202                               1232
      |Cadherin EC
GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

xxx|                               1292
GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu

1322                               1352
AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala

1382                               1412
AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442                               1472
AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser
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FIG. 2B (cont.)

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1502 1532
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn

1562 1592
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1622 1652
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp

1682 1712
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1742 1772
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1802 1832
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1862 1892
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val

1922 1952 |XXXXXXXXXXXXXXXXXXXXX
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1982 XXXXXXXXXXXX deleted in CLASP-2D(KIAA1058) XXXXXXXXXXXXXXXXXXXXXXXX |
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2042 2072
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2102 2132
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

2162 2192 Deleted
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC |xxx
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

in HC2B 2252
xxx|
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

FIG. 2B (cont.)

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2282                                2312
TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342                                2372
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402                                2432
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462                                2492
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522                                2552
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582                                2612
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642                                2672
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702                                2732
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762                                2792
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822                                2852
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

```

[Additional and differential exon usage found at position 2927 consisting of 69 nucleotides. This entire sequence is found in Human CLASP-2D (KIAA1058) and not other isoforms of CLASP-2. It has a sequence of:
AAGCAGTCCAGTGGGAGCCGCCCTTCTCCCCACAGCCATAGCGCCTGCCTGAGGAGGCCGGGGAG]

Transmembrane Domain |XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX|
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

```

2942                                2972
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu

```

FIG. 2B (cont.)

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3002 |xx Sequence deleted in CLASP-2E xxxxx
 GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG
 asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx 3092
 TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT
 cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

[Additional and differential exon usage found at position 3153. The entire sequence below is found in Human CLASP-2D. Underlined sequence is found in Human CLASP-2B, 2C and 2E.

TGAGAGGCTGGCCCATCTGTATGACACGCTGCACCGGGCTACAGCAAAGTGACCGAGGTCAT
GCACTCGGGCCGACGGCTTCTGGGGACCTACTCCGGGTAGCCTTCTTCGGGCAGGCAGCGCAATACCAGTTT
ACAGACAGTGAAACAGATGTGGAGGGATT]

3122 3155
 ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT
 ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

3182 3212
 ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG
 ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu

3242 3272
 TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC
 tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

3302 3332
 CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT
 pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3362 3392
 GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC
 asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

3422 3452
 TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG
 phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln

3482 3512
 TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC
 cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys lys arg ile

Two nucleotide deletion (nts 3586 and 3587) found in Human CLASP-2C

3542 3572 |xxx|
 CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG
 pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

FIG. 2B (cont.)

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3602 3632
AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA
ser lys lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys

3662 3692
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3722 3752
GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG
ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

3782 3812
CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu

3842 3872
CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA
arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

Insertion of 8 nucleotides found only in Human CLASP-2D with sequence: CTGGGATG

3902 3932
ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962 3992
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022 |xxxxx PBM xxxxx|
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG
met val his gly met thr ser ser ser val val STP

4082 4112
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142 4172
ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202 4232
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262 4292
GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322 4352
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382 4412
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

FIG. 2B (cont.)

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4442	4472
CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA	TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA
4502	4532
GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT	ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA
4562	4592
TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT	AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT
4622	4652
GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT	ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC
4682	4712
TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG	TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA
4742	4772
ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA	AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC
4802	
TTT ACT	

FIG. 2B (cont.)

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058
HC2E
HC2F

GCATCTGGAAATCTTGACAAAAATGCCAGATTTTCTGCCATCTACAGGCAAGACAGCAAT

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058
HC2E
HC2F

AAGCTATCCAATGATGACATGCTCAAGTTACTTGCAGACTTTCGGAAACCTGAGAAGATG

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058
HC2E
HC2F

GCTAAGCTCCCGAGTGATTTTAGGCAATCTAGACATTACAATTGATAATGTTTCCTCAGAC

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058
HC2E
HC2F

TTCCCTAATTATGTTAATTCATCATACATTCCCACAAAACAATTTGAAACCTGCAGTAAA

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058
HC2E
HC2F

ACTCCCATCACGTTTGAAGTGGAGGAATTTGTGCCCTGCATACCAAAACACACTCAGCCT

FIG. 3A

HC2A
 HC2-80
 HC2B
 HC2C
 HC2D-KIAA1058
 HC2E
 HC2F

 TACACCATCTACACCAATCACCTTTACGTTTATCCTAAGTACTTGAAATACGACAGTCAG

HC2A
 HC2-80
 HC2B
 HC2C
 HC2D-KIAA1058
 HC2E
 HC2F

 AAGTCTTTTGCCAAGGCTAGAAATATTGCGATTTGCATTGAATTCAAAGATTCAGATGAG

HC2A
 HC2-80
 HC2B
 HC2C
 HC2D-KIAA1058
 HC2E
 HC2F

 GAAGACTCTCAGCCCCCTTAAGTGCATTTATGGCAGACCTGGTGGGCCAGTTTTCACAAGA

HC2A
 HC2-80
 HC2B
 HC2C
 HC2D-KIAA1058
 HC2E
 HC2F

-----AGTTTACACCATCACCAAACCCAGAATTTTATGATGAGATTAAA

 AGCGCCTTTGCTGCAGTTTACACCATCACCAAACCCAGAATTTTATGATGAGATTAAA

HC2A
 HC2-80
 HC2B
 HC2C
 HC2D-KIAA1058
 HC2E
 HC2F

ATAGAGTTGCCCACTCAGCTGCATGAAAAGCACCACTGTTGCTCACATTCTTCCATGTC

 ATAGAGTTGCCCACTCAGCTGCATGAAAAGCACCACTGTTGCTCACATTCTTCCATGTC

HC2A
 HC2-80
 HC2B
 HC2C
 HC2D-KIAA1058
 HC2E
 HC2F

AGCTGTGACAACTCAAGTAAAGGAAGCACGAAGAAGAGGGATGTCGTTGAAACCCAAGTT

 AGCTGTGACAACTCAAGTAAAGGAAGCACGAAGAAGAGGGATGTCGTTGAAACCCAAGTT

FIG. 3A (cont.)

HC2A	GGCTACTCCTGGCTTCCCTTCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATC
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GGCTACTCCTGGCTTCCCTTCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATC
HC2E	-----
HC2F	-----

HC2A	CCGGTCTCGGCGAACCTTCCTTCGGGCTATCTTGGCTACCAAGAGCTTGGGATGGGCAGG
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CCGGTCTCGGCGAACCTTCCTTCGGGCTATCTTGGCTACCAAGAGCTTGGGATGGGCAGG
HC2E	-----
HC2F	-----

HC2A	CATTATGGTCCGGAAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CATTATGGTCCGGAAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACT
HC2E	-----
HC2F	-----

HC2A	CATCTGGTTTCTACAGTGATACTCAGGATCAGCATTTACATAATTTTTTCCAGTACTGT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CATCTGGTTTCTACAGTGATACTCAGGATCAGCATTTACATAATTTTTTCCAGTACTGT
HC2E	-----
HC2F	-----

HC2A	CAGAAAACCGAATCTGGAGCCCAAGCCTTAGGAAACGAACCTGTAAAGTACCTTAAGAGT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CAGAAAACCGAATCTGGAGCCCAAGCCTTAGGAAACGAACCTGTAAAGTACCTTAAGAGT
HC2E	-----
HC2F	-----

HC2A	CTGCATGCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2-80	-----
HC2B	-----GCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2C	-----
HC2D-KIAA1058	CTGCATGCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2E	-----GCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2F	-----

FIG. 3A (cont.)

HC2A	TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2-80	-----
HC2B	TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2C	-----
HC2D-KIAA1058	TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2E	TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2F	-----
HC2A	ATTCATGTGGTTGCCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2-80	-----
HC2B	ATTCATGTGGTTGCCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2C	-----
HC2D-KIAA1058	ATTCATGTGGTTGCCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2E	ATTCATGTGGTTGCCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2F	-----
HC2A	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2-80	-----
HC2B	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2C	-----
HC2D-KIAA1058	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2E	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2F	-----
HC2A	CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCCCTCACCAGCAACAAA
HC2-80	-----
HC2B	CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCCCTCACCAGCAACAAA
HC2C	-----
HC2D-KIAA1058	CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCCCTCACCAGCAACAAA
HC2E	CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCCCTCACCAGCAACAAA
HC2F	-----
HC2A	CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2-80	-----
HC2B	CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2C	-----
HC2D-KIAA1058	CTACTGAAGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2E	CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2F	-----
HC2A	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCCTGCATCCTATCATCAT
HC2-80	-----
HC2B	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCCTGCATCCTATCATCAT
HC2C	-----
HC2D-KIAA1058	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCCTGCATCCTATCATCAT
HC2E	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCCCTGCATCCTATCATCAT
HC2F	-----

FIG. 3A (cont.)

HC2A	GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2-80	-----
HC2B	GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2C	-----
HC2D-KIAA1058	GCAGTGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2E	GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2F	-----
HC2A	CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2-80	-----
HC2B	CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2C	-----
HC2D-KIAA1058	CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2E	CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2F	-----
HC2A	TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACCTACATTAGCTGTTTTGCTCCT
HC2-80	-----
HC2B	TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACCTACATTAGCTGTTTTGCTCCT
HC2C	-----
HC2D-KIAA1058	TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACCTACATTAGCTGTTTTGCTCCT
HC2E	TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACCTACATTAGCTGTTTTGCTCCT
HC2F	-----
HC2A	GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2-80	-----
HC2B	GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2C	-----
HC2D-KIAA1058	GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2E	GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2F	-----
HC2A	GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2-80	-----
HC2B	GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2C	-----
HC2D-KIAA1058	GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2E	GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2F	-----
HC2A	CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2-80	-----TCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2B	CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2C	-----
HC2D-KIAA1058	CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2E	CAAGACCTCCAGCTTGACTACTCATTAAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2F	-----

FIG. 3A (cont.)

HC2A	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2-80	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2B	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2C	-----
HC2D-KIAA1058	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2E	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2F	-----
HC2A	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2-80	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2B	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2C	-----
HC2D-KIAA1058	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2E	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2F	-----
HC2A	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2-80	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2B	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2C	-----
HC2D-KIAA1058	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2E	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2F	-----
HC2A	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC
HC2-80	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC
HC2B	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC
HC2C	-----
HC2D-KIAA1058	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACT
HC2E	AACGTCCAGCGGATCAATGTGAGGGATGTGTACCCCTTCCCTGTGAACGCGGGCATGACC
HC2F	-----
HC2A	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2-80	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2B	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2C	-----
HC2D-KIAA1058	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2E	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGCAGAAGGGA
HC2F	-----
HC2A	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2-80	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2B	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2C	-----
HC2D-KIAA1058	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2E	AGCACCCCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2F	-----

FIG. 3A (cont.)

HC2A	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2-80	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2B	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2C	-----
HC2D-KIAA1058	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2E	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2F	-----GCTGATTTCGAGAGGATCT
HC2A	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2-80	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2B	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2C	-----
HC2D-KIAA1058	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2E	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2F	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2A	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2-80	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2B	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2C	-----
HC2D-KIAA1058	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2E	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2F	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2A	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCCTCTACATCTTAAAGAGCATGTCT
HC2-80	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCCTCTACATCTTAAAGAGCATGTCT
HC2B	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCCTCTACATCTTAAAGAGCATGTCT
HC2C	-----
HC2D-KIAA1058	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCCTCTACATCTTAAAGAGCATGTCT
HC2E	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCCTCTACATCTTAAAGAGCATGTCT
HC2F	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCCTCTACATCTTAAAGAGCATGTCT
HC2A	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2-80	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2B	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2C	-----
HC2D-KIAA1058	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2E	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2F	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2A	ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG
HC2-80	ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG
HC2B	ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG
HC2C	-----
HC2D-KIAA1058	ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG
HC2E	ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG
HC2F	ACAATATCTGAAGTCTGCCTGCACCAGTTCCAGTACATGGGGAAGCGATACATAGCCAGG

FIG. 3A (cont.)

HC2A	AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2-80	AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2B	AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2C	-----AA-----
HC2D-KIAA1058	AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2E	-----TGTGA-----GAAAG-----ATATCAAGTGT----
HC2F	
HC2A	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2-80	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2B	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2C	-----CAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2D-KIAA1058	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2E	-----GCTTGGA-----
HC2F	
HC2A	CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2-80	CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2B	CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2C	-----
HC2D-KIAA1058	CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2E	CTCACTTTTAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2F	-TTTCTGTAGACAATGGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2A	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTTCTCTATTTACA
HC2-80	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTTCTCTATTTACA
HC2B	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTTCTCTATTTACA
HC2C	-----
HC2D-KIAA1058	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTTCTCTATTTACA
HC2E	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTTCTCTATTTACA
HC2F	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTTCTCTATTTACA
HC2A	TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2-80	TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2B	TTGGCGTTTAAG-----CTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2C	-----
HC2D-KIAA1058	TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2E	TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2F	TTGGCGTTTAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2A	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2-80	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2B	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2C	-----
HC2D-KIAA1058	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2E	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2F	A-----

FIG. 3A (cont.)

HC2A	TTCAC TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2-80	TTCAC TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2B	TTCAC TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2C	-----
HC2D-KIAA1058	TTCAC TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2E	TTCAC TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2F	-----
HC2A	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACTCCAAGCTGAGCTCC
HC2-80	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACTCCAAGCTGAGCTCC
HC2B	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACTCCAAGCTGAGCTCC
HC2C	-----
HC2D-KIAA1058	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACTCCAAGCTGAGCTCC
HC2E	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTAACTCCAAGCTGAGCTCC
HC2F	-----
HC2A	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT
HC2-80	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT
HC2B	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT
HC2C	-----
HC2D-KIAA1058	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT
HC2E	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACAACCTTTGATTACACT
HC2F	-----
HC2A	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTGTCAGCCAGCTGATA
HC2-80	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTGTCAGCCAGCTGATA
HC2B	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTGTCAGCCAGCTGATA
HC2C	-----
HC2D-KIAA1058	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTGTCAGCCAGCTGATA
HC2E	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGTGTCAGCCAGCTGATA
HC2F	-----
HC2A	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2-80	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2B	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2C	-----
HC2D-KIAA1058	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2E	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2F	-----
HC2A	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2-80	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2B	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2C	-----
HC2D-KIAA1058	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2E	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2F	-----

FIG. 3A (cont.)

HC2A	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCAGATGAAGGAGCATGAGAACGAC
HC2-80	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCAGATGAAGGAGCATGAGAACGAC
HC2B	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCAGATGAAGGAGCATGAGAACGAC
HC2C	-----
HC2D-KIAA1058	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCAGATGAAGGAGCATGAGAACGAC
HC2E	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCAGATGAAGGAGCATGAGAACGAC
HC2F	-----
HC2A	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2-80	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2B	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2C	-----
HC2D-KIAA1058	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2E	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2F	-----
HC2A	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2-80	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2B	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2C	-----
HC2D-KIAA1058	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2E	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2F	-----
HC2A	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2-80	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2B	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2C	-----
HC2D-KIAA1058	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2E	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCTAGTGGCAGAATATCTCACACGGAAA
HC2F	-----
HC2A	G-----
HC2-80	G-----
HC2B	G-----
HC2C	-----
HC2D-KIAA1058	GAAGCAGTCCAGTGGGAGCCGCCCTTCTCCCCACAGCCATAGCGCCTGCCTGAGGAGG
HC2E	G-----
HC2F	-----
HC2A	-----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2-80	-----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2B	-----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2C	-----GTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2D-KIAA1058	AGCCGGGGAGGCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2E	-----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2F	-----

FIG. 3A (cont.)

HC2A GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
 HC2-80 GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
 HC2B GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
 HC2C GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
 HC2D-KIAA1058 GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
 HC2E GACGAGGAGGCCTCCATGATGGAAGACGTGGGGA-----
 HC2F -----

HC2A GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG
 HC2-80 GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG
 HC2B GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG
 HC2C GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG
 HC2D-KIAA1058 GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAGCCGAGCGCTACGAG
 HC2E -----AAGCCGAGCGCTACGAG
 HC2F -----

HC2A CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCCGAGGGATTT-----
 HC2-80 CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCCGAGGGATTT-----
 HC2B CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCCGAGGGATTTTGAG
 HC2C CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCCGAGGGATTTTGAG
 HC2D-KIAA1058 CTCATTGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCCGAGGGATTTTGAG
 HC2E CTCATCGCCGACATCTACAACTTATCATCCCCATTTATGAGAAGCCGAGGGATTTTGAG
 HC2F -----

HC2A -----
 HC2-80 -----
 HC2B AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
 HC2C AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
 HC2D-KIAA1058 AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
 HC2E AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
 HC2F -----

HC2A -----
 HC2-80 -----
 HC2B CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG-----
 HC2C CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG-----
 HC2D-KIAA1058 CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGGCGC
 HC2E CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG-----
 HC2F -----

HC2A -----CTTTGAAGATGAAGATGGA
 HC2-80 -----CTTTGAAGATGAAGATGGA
 HC2B -----GATTCTTTGAAGATGAAGATGGA
 HC2C -----GATTCTTTGAAGATGAAGATGGA
 HC2D-KIAA1058 CAATACCAGTTTACAGACAGTGAAACAGATGTGGAGGGATTCTTTGAAGATGAAGATGGA
 HC2E -----GATTCTTTGAAGATGAAGATGGA
 HC2F -----

FIG. 3A (cont.)

HC2A AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTCGGAAATTTCTCAGAGACTC
 HC2-80 AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTCGGAAATTTCTCAGAGACTC
 HC2B AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTCGGAAATTTCTCAGAGACTC
 HC2C AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTCGGAAATTTCTCAGAGACTC
 HC2D-KIAA1058 AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTCGGAAATTTCTCAGAGACTC
 HC2E AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTCGGAAATTTCTCAGAGACTC
 HC2F -----

HC2A CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
 HC2-80 CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
 HC2B CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
 HC2C CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
 HC2D-KIAA1058 CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
 HC2E CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
 HC2F -----

HC2A AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
 HC2-80 AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
 HC2B AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
 HC2C AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
 HC2D-KIAA1058 AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCCTACATCCAGGTGACTCACGTCATC
 HC2E AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
 HC2F -----

HC2A CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCAACAAC
 HC2-80 CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCAACAAC
 HC2B CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCAACAAC
 HC2C CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCAACAAC
 HC2D-KIAA1058 CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCAACAAC
 HC2E CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAACAGAGTTTGAGAGATCCCAACAAC
 HC2F -----

HC2A ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
 HC2-80 ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
 HC2B ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
 HC2C ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
 HC2D-KIAA1058 ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
 HC2E ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
 HC2F -----

HC2A GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
 HC2-80 GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
 HC2B GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
 HC2C GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
 HC2D-KIAA1058 GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
 HC2E GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
 HC2F -----

FIG. 3A (cont.)

HC2A	AAGCGCATCCCTGTTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2-80	AAGCGCATCCCTGTTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2B	AAGCGCATCCCTGTTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2C	AAGCGCATCCCTTTTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGT--CCATT
HC2D-KIAA1058	AAGCGCATCCCTGTTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2E	AAGCGCATCCCTGTTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2F	-----
HC2A	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2-80	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2B	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2C	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2D-KIAA1058	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2E	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2F	-----
HC2A	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA
HC2-80	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA
HC2B	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA
HC2C	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA
HC2D-KIAA1058	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA
HC2E	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA
HC2F	-----
HC2A	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2-80	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2B	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2C	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2D-KIAA1058	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2E	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2F	-----
HC2A	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2-80	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2B	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2C	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2D-KIAA1058	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2E	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2F	-----
HC2A	GTAAACGAACGCTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAAC
HC2-80	GTAAACGAACGCTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAAC
HC2B	GTAAACGAACGCTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAAC
HC2C	GTAAACGAACGCTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAAC
HC2D-KIAA1058	GTAAACGAACGCTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAAC
HC2E	GTAAACGAACGCTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAAC
HC2F	-----

FIG. 3A (cont.)

HC2A	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2-80	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2B	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2C	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2D-KIAA1058	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAGCTGGGATGATCTGCC
HC2E	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2F	-----
HC2A	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2-80	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2B	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2C	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2D-KIAA1058	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2E	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2F	-----
HC2A	GGACTCCAACAAGCACAATGGTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2-80	GGACTCCAACAAGCACAATGGTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2B	GGACTCCAACAAGCACAATGGTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGA----
HC2C	GGACTCCAACAAGCACAATGGTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGA----
HC2D-KIAA1058	GGACTCCAACAAGCACAATGGTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2E	GGACTCCAACAAGCACAATGGTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGA----
HC2F	-----
HC2A	ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTGCAATTGCAAACTCAGGATGCTTTCCAA
HC2-80	ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTGCAATTGCAAACTCAGGATGCTTTCCAA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTGCAATTGCAAACTCAGGATGCTTTCCAA
HC2E	-----
HC2F	-----
HC2A	AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCAAGGGGAAGGGGAGAGAAAGGAAA
HC2-80	AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCAAGGGGAAGGGGAGAGAAAGGAAA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCA-GGGGAAGGGGAGAGAAAGGAAA
HC2E	-----
HC2F	-----
HC2A	TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT
HC2-80	TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A	TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTTCATTGTGTCTTAACAAAGGTGTGGTA
HC2-80	TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTTCATTGTGTCTTAACAAAGGTGTGGTA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTTCATTGTGTCTTAACAAAGGTGTGGTA
HC2E	-----
HC2F	-----
HC2A	GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTTAGAATAGATG
HC2-80	GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTTAGAATAGATG
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTTAGAATAGATG
HC2E	-----
HC2F	-----
HC2A	GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2-80	GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2E	-----
HC2F	-----
HC2A	GCCTGGGGGACCTTTTGCCTCGACTCGTGCCGAAATCTGATCGTAATCAGGGTACAGAA
HC2-80	GCCTGGGGGACCTTTTGCCTCGACTCGTGCCGAAATCTGATCGTAATCAGGGTACAGAA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GCCTGGGGGACCTTTTGCCTCGAGGCTGAGCTGGAAAATCTTGAAAATATTTTTTT---T
HC2E	-----
HC2F	-----
HC2A	CTTACTAGTTTTGTCTAGGAGTATGTTGTATGACTAGGATTTGTGCTATTATCTCATTCA
HC2-80	CTTACTAGTTTTGTCTAGGAGTATGTTGTATGACTAGGATTTGTGCTATTATCTCATTCA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TTTCCTGTGGCACATTCAGGTTGAATACAAGAACTATTTTTGTGACTAGTTTTTGTATGAC
HC2E	-----
HC2F	-----
HC2A	ACAACATAGAGCAAGAATAGTGAGCTAACTGAGCTAGACACTCAATTAATCCGCTACTGG
HC2-80	ACAACATAGAGCAAGAATAGTGAGCTAACTGAGCTAGACACTCAATTAATCCGCTACTGG
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CTAAGGGAAGTACCATTGTAATTTTTGTACCAGTGAACCAGGAGATTTAGTGCTTTTAT
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A CTTCAAGTCAGAACTTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
 HC2-80 CTTCAAGTCAGAACTTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
 HC2B -----
 HC2C -----
 HC2D-KIAA1058 ATTCAATTCCTTGCAATTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAACT
 HC2E -----
 HC2F -----

HC2A TTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAATTGTGATAAATTTGTG
 HC2-80 TTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAATTGTGATAAATTTGTG
 HC2B -----
 HC2C -----
 HC2D-KIAA1058 AGTCAAGCAGTTTAGAACCAAAGGCCTATATTAATAACCGCAACTATGCTGAAAAGTACA
 HC2E -----
 HC2F -----

HC2A CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTCATAAAAATGTGCAATAT
 HC2-80 CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTCATAAAAATGTGCAATAT
 HC2B -----
 HC2C -----
 HC2D-KIAA1058 AAGTAGTACAGTATATTGTTATGTACATATCATTGTTAATACAGTCCTGGCATTCTGTAC
 HC2E -----
 HC2F -----

HC2A GGAGATGTATACAAGTCCTTTACT-----
 HC2-80 GGAGATGTATACAAGTCCTTTACT-----
 HC2B -----
 HC2C -----
 HC2D-KIAA1058 ATATATGTATTACATTTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAAT
 HC2E -----
 HC2F -----

HC2A -----
 HC2-80 -----
 HC2B -----
 HC2C -----
 HC2D-KIAA1058 TGTGATAAATTTGTGCTGTTCCAGTATATGCAATACACTTTAATGTTTTATTCTTGTACA
 HC2E -----
 HC2F -----

HC2A -----
 HC2-80 -----
 HC2B -----
 HC2C -----
 HC2D-KIAA1058 TAAAAATGTGCAATATGGAGATGTATACAGTCCTTTACTATATTAGGTTTATAAACAGTTT
 HC2E -----
 HC2F -----

FIG. 3A (cont.)

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TAAGAATTTCATCCTTTTGCCAAAATGGTGGAGTATGTAATTGGTAAATCATAAATCCTG
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TGGTGAATGGTGGTGTACTTTAAAGCTGTCACCATGTTATATTTTCTTTTAAGACATTAA
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TTTAGTAATTTTATATTTGGGAAAATAAAGGTTTTTAATTTTATTTAACTGGAATCACTG
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CCCTGCTGTAATTAAACATTCTGTACCACATCTGTATTAAAAAGACATTGCTGACC
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A	CTTCAAGTCAGAACTTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
HC2-80	CTTCAAGTCAGAACTTTGTCATTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATTCATTTCCCTTGCAATTTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAACT
HC2E	-----
HC2F	-----
HC2A	TTCTACATTTTAAATACTCACATGGGCTTATGCATTAAGTTTAAATTGTGATAAAATTGTG
HC2-80	TTCTACATTTTAAATACTCACATGGGCTTATGCATTAAGTTTAAATTGTGATAAAATTGTG
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AGTCAAGCAGTTTAGAACCAAAGGCCTATATTAATAACCGCAACTATGCTGAAAAGTACA
HC2E	-----
HC2F	-----
HC2A	CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTCATAAAAATGTGCAATAT
HC2-80	CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTCATAAAAATGTGCAATAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AAGTAGTACAGTATATTGTTATGTACATATCATTGTTAATACAGTCCTGGCATTCTGTAC
HC2E	-----
HC2F	-----
HC2A	GGAGATGTATACAAGTCTTTACT-----
HC2-80	GGAGATGTATACAAGTCTTTACT-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATATATGTATTACATTTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAAAT
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TGTGATAAATTTGTGCTGTTCCAGTATATGCAATACACTTTAATGTTTTATTCTTGTTACA
HC2E	-----
HC2F	-----
HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TAAAAATGTGCAATATGGAGATGTATACAGTCTTTACTATATTAGGTTTATAAACAGTTT
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058
HC2E
HC2F

TAAGAATTTTCATCCTTTTGCCAAAATGGTGGAGTATGTAATTGGTAAATCATAAATCCTG

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058
HC2E
HC2F

TGGTGAATGGTGGTGTACTTTTAAAGCTGTCACCATGTTATATTTTCTTTTAAGACATTAA

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058
HC2E
HC2F

TTTAGTAATTTTATATTTGGGAAAATAAAGGTTTTTAATTTTATTAACTGGAATCACTG

HC2A
HC2-80
HC2B
HC2C
HC2D-KIAA1058
HC2E
HC2F

CCCTGCTGTAATTAAACATTCTGTACCACATCTGTATTAAAAAGACATTGCTGACC

HC2A	-----
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	ASGNLDKNARFSAIYRQDSNKLSDNDMLKLIADFRKPEKMAKLPVILGNLDITIDNVSSD
HC2E	-----
HC2F	-----
HC2A	-----
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVPKYLKYDSQ
HC2E	-----
HC2F	-----
HC2A	-----VLHHHQNPFEFYDEIK
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	KSAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTSAFAAVLHHHQNPFEFYDEIK
HC2E	-----
HC2F	-----
HC2A	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
HC2E	-----
HC2F	-----
HC2A	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
HC2E	-----
HC2F	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2A-80	-----
HC2B	-----AMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2C	-----
HC2D	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2E	-----AMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2F	-----

Fig. 3B

HC2A	IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSTNK
HC2A-80	-----
HC2B	IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSTNK
HC2C	-----
HC2D	IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSTNK
HC2E	IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSTNK
HC2F	-----
HC2A	LLRYSWFFFDVLIKSMQHLIENSKVKLLRNQRFPPASYHHAAETVVNMLMPHITQKFGDN
HC2A-80	-----
HC2B	LLRYSWFFFDVLIKSMQHLIENSKVKLLRNQRFPPASYHHAAETVVNMLMPHITQKFGDN
HC2C	-----
HC2D	LLKYSWFFFDVLIKSMQHLIENSKVKLLRNQRFPPASYHHAAETVVNMLMPHITQKFRDN
HC2E	LLRYSWFFFDVLIKSMQHLIENSKVKLLRNQRFPPASYHHAAETVVNMLMPHITQKFGDN
HC2F	-----
HC2A	PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2A-80	-----
HC2B	PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2C	-----
HC2D	PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2E	PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2F	-----
HC2A	EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTLQEFREVRLI
HC2A-80	-----QLDYSLTDEFCRNHFLVGLLLREVGTLQEFREVRLI
HC2B	EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTLQEFREVRLI
HC2C	-----
HC2D	EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTLQEFREVRLI
HC2E	EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTLQEFREVRLI
HC2F	-----
HC2A	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2A-80	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2B	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2C	-----
HC2D	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2E	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2F	-----
HC2A	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2A-80	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2B	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2C	-----
HC2D	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2E	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2F	-----ADSRGS

FIG. 3B (cont.)

HC2A	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLIMCFLYILKSMS
HC2A-80	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLIMCFLYILKSMS
HC2B	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLIMCFLYILKSMS
HC2C	-----
HC2D	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLIMCFLYILKSMS
HC2E	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLIMCFLYILKSMS
HC2F	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLIMCFLYILKSMS
HC2A	DDALFTYWNKASTSEIMDFFTISEVCLHQFYQYMGKRYIARNQEGLGPIVHDKRSQTLFVS
HC2A-80	DDALFTYWNKASTSEIMDFFTISEVCLHQFYQYMGKRYIARNQEGLGPIVHDKRSQTLFVS
HC2B	DDALFTYWNKASTSEIMDFFTISEVCLHQFYQYMGKRYIARNQEGLGPIVHDKRSQTLFVS
HC2C	-----
HC2D	DDALFTYWNKASTSEIMDFFTISEVCLHQFYQYMGKRYIAR-----
HC2E	DDALFTYWNKASTSEIMDFFTISEVCLHQFYQYMGKRYIARNQEGLGPIVHDKRSQTLFVS
HC2F	DDALFTYWNKASTSEIMDFFTISEVCLHQFYQYMGKRYIAS-----VR--KISSVLGIS
HC2A	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2A-80	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2B	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2C	-----
HC2D	---TGMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2E	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2F	V-----D-NG-----YGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2A	LAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2A-80	LAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2B	LAFK--LLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2C	-----
HC2D	LAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2E	LAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRA
HC2F	LAFKNQLLADHGHNPMLKKK-----
HC2A	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVII SVSqli
HC2A-80	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVII SVSqli
HC2B	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVII SVSqli
HC2C	-----
HC2D	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVII SVSqli
HC2E	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVII SVSqli
HC2F	-----
HC2A	ADVVGIGETRFQQSLSIINNCANSRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2A-80	ADVVGIGETRFQQSLSIINNCANSRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2B	ADVVGIGETRFQQSLSIINNCANSRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2C	-----
HC2D	ADVVGIGETRFQQSLSIINNCANSRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2E	ADVVGIGETRFQQSLSIINNCANSRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2F	-----

FIG. 3B (cont.)

HC2A	PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV TALVAEYLTRK
HC2A-80	PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV TALVAEYLTRK
HC2B	PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV TALVAEYLTRK
HC2C	-----
HC2D	PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV TALVAEYLTRK
HC2E	PEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV TALVAEYLTRK
HC2F	-----
HC2A	-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2A-80	-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2B	-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2C	-----FRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2D	EAVQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2E	-----GVFRQGCTAFRVITPNIDEEASMMEDVG-----
HC2F	-----
HC2A	DVIMELLEQCADGLWKAERYELIADIYKLIIP IYEKRR-----
HC2A-80	DVIMELLEQCADGLWKAERYELIADIYKLIIP IYEKRR-----
HC2B	DVIMELLEQCADGLWKAERYELIADIYKLIIP IYEKRRD FERLAHLYDTLHRAYSK
HC2C	DVIMELLEQCADGLWKAERYELIADIYKLIIP IYEKRRD FERLAHLYDTLHRAYSK
HC2D	DVIMELLEQCADGLWKAERYELIADIYKLIIP IYEKRRD FERLAHLYDTLHRAYSK
HC2E	-----KAERYELIADIYKLIIP IYEKRRD FERLAHLYDTLHRAYSK
HC2F	-----
HC2A	-----DFFEDEDGKEYIYKEPKLTPLSE
HC2A-80	-----DFFEDEDGKEYIYKEPKLTPLSE
HC2B	VTEVMHSGRRLLGTYFRVAFFG-----QGFFEDEDGKEYIYKEPKLTPLSE
HC2C	VTEVMHSGRRLLGTYFRVAFFG-----QGFFEDEDGKEYIYKEPKLTPLSE
HC2D	VTEVMHSGRRLLGTYFRVAFFGQAAQYQFTDSETDVEGFFEDEDGKEYIYKEPKLTPLSE
HC2E	VTEVMHSGRRLLGTYFRVAFFG-----QGFFEDEDGKEYIYKEPKLTPLSE
HC2F	-----
HC2A	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLD SKYAYIQVTHVIPFFDEKELQERKTEF
HC2A-80	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLD SKYAYIQVTHVIPFFDEKELQERKTEF
HC2B	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLD SKYAYIQVTHVIPFFDEKELQERKTEF
HC2C	ISQRLLKLYSDKFGSENVKMTQDSGKVNPKDLD SKYAYIQVTHVIPFFDEKELQERKTEF
HC2D	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLD SKYAYIQVTHVIPFFDEKELQERKTEF
HC2E	ISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLD SKYAYIQVTHVIPFFDEKELQERKTEF
HC2F	-----
HC2A	ERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRR TILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2A-80	ERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRR TILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2B	ERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRR TILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2C	ERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRR TILTAIHCFPYVKKRIPFMYQHHTDLNP
HC2D	ERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRR TILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2E	ERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRR TILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2F	-----

FIG. 3B (cont.)

HC2A	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKR
HC2A-80	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKR
HC2B	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKR
HC2C	IEVHZ-----
HC2D	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKR
HC2E	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKR
HC2F	-----
HC2A	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2A-80	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2B	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2C	-----
HC2D	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2E	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2F	-----
HC2A	ICPLEEKTSVLPNSLHIFNAISGTPPTSTMVHGMTSSSSSVVZ----
HC2A-80	ICPLEEKTSVLPNSLHIFNAISGTPPTSTMVHGMTSSSSSVVZ----
HC2B	ICPLEEKTSVLPNSLHIFNAISGTPPTSTMVHGMTSSSSSVVZ----
HC2C	-----
HC2D	LG-----
HC2E	ICPLEEKTSVLPNSLHIFNAISGTPPTSTMVHGMTSSSSSVVZ----
HC2F	-----

FIG. 3B (cont.)

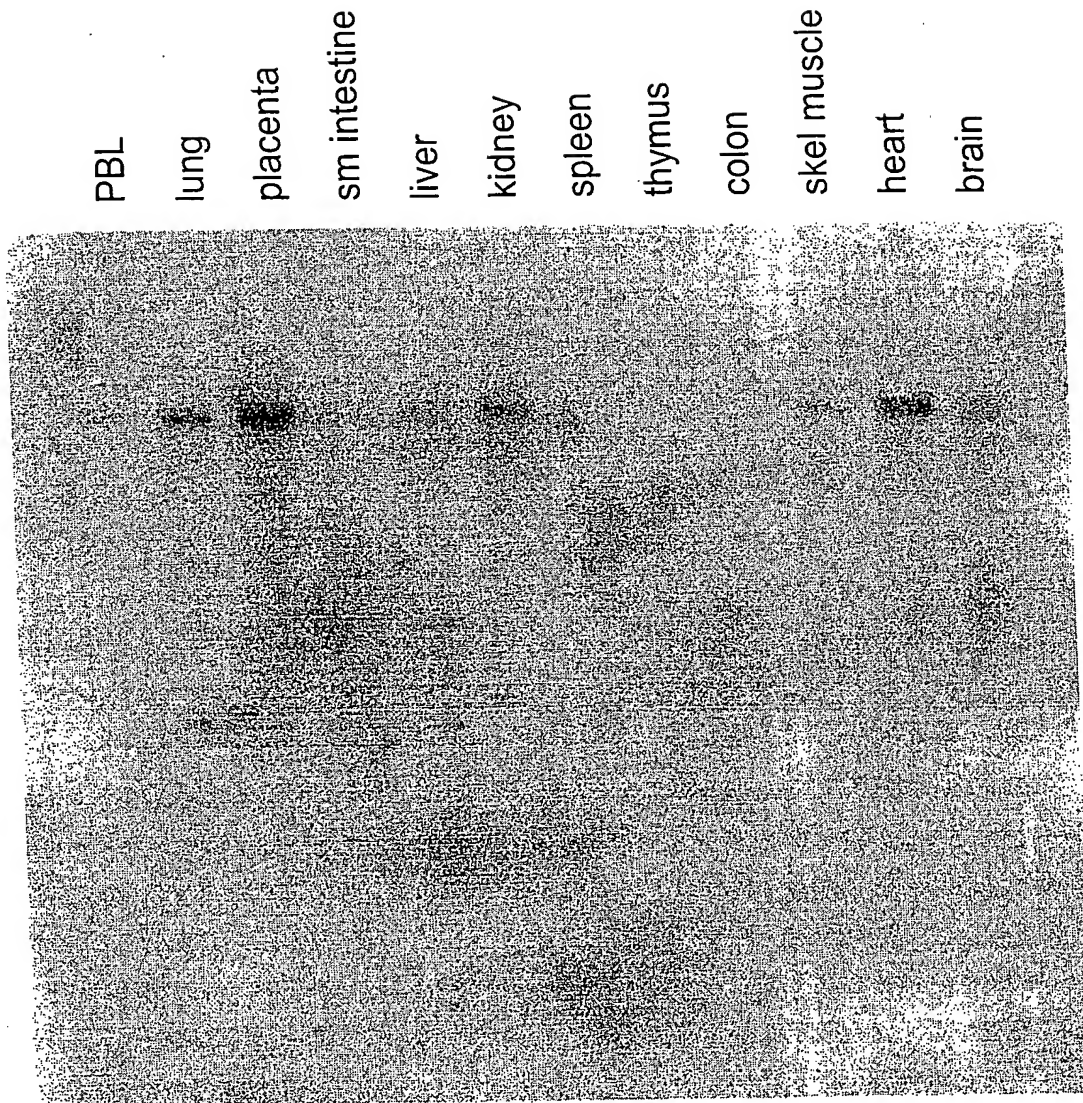


FIG. 4A

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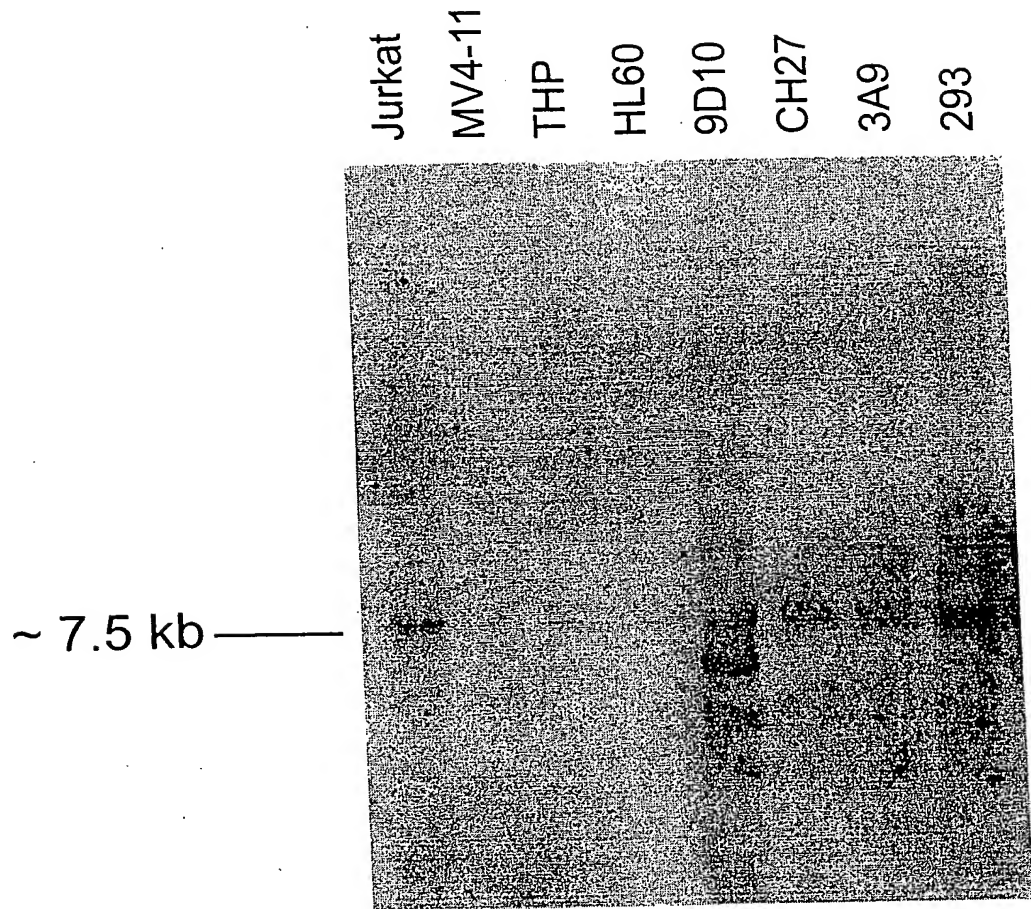


FIG. 4B

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSDNDMLKLLADFRKPEKMAKLEPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPFEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVETRSAFAAVLHHHQNPFEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGYQELGMRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA	PVSANLPSGYLGYQELGMRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIREFLSVIILMQLFWVLPNMIHEDDVPI SCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSPSPSAES
HC5	-----

FIG.5A

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HC2A	I IHVVAQCHEEGLESHLSYVVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
KIAA	I IHVVAQCHEEGLESHLSYVVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
rat	-----
HC4	LFHIVSKCHEEGLD SYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK
HC3	TQAMDRSCNRMSHTETSSFLQTLTGRLP-----TKKLFHEELALQWVVCSG--SVR---E
HC5	-----
	Cadherin
	Cleavage
HC2A	KLLRYSWFFFDVLIK SMAQH LIENSKVKLI RNQRF PASYHHAETVVNMLMPHITQKFGD
KIAA	KLLKYSWFFFDVLIK SMAQH LIENSKVKLI RNQRF PASYHHAETVVNMLMPHITQKFRD
rat	-----
HC4	KLLKYSWFFFEIIAKSMATYLL ENKIKLTHGQRF PKAYHHAHLSLFLAIT-IVESQYAE
HC1	HVLKHSWFFFAIILKSMAQH LIDTNKIQLR PQRF PESYQNELDNLMVLSDHVIWKYKD
HC3	SALQQAWFFFEIMVKSMVHHLYFNDKLEA RKS RFPERFMDIAALVSTIASDIVSRFQK
HC5	-----
HC2A	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat	-----
HC4	IPKESRNVNYSLASFLKCCLTLM DRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1	ALEETRRATHSVAREFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTL CQYKDFDL
HC3	DTEMVERLNTSLAFFLNDLLSVM DRGFVFSLIKSCYQVSSKLYSLPNPSVLVSLRLDFL
HC5	-----
HC2A	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF
KIAA	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF
rat	-----
HC4	QTICNHEHYIPLNLPM-----AFAPKPLQR-----VQDSNL---EYSLSDEY
HC1	QEVQCHEHFIPCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF
HC3	RIICSHHYVTNLNLP CSLLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF
HC5	-----MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA
HC2A	CRNHFLVGLLLREVGTALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA	CRNHFLVGLLLREVGTALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat	-----
HC4	CKHHFLVGLLLRETSIALQDNYE---IRYTAISVIKNLLIKHAFDTRYQHKNQQA KIAQ
HC1	CRKHFLIGILLREVGFALQEDQD---VRHLALAVLKNLMAKHSFDDRYEPRKQAQIAS
HC3	RQQHYLAGLVLT ELAVILDPDAEGLFGLHKKVINMVHNLSSHSDSDPRYSDPQIKARVAM
HC5	SSTS-SPGLLFT ELAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAA
HC2A	LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA	LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat	-----
HC4	LYLPPFVGLLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
HC1	LYMPLYGMLLDNMPRIYKLDLYPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDT SFS
HC3	LYLPLIGIIMETVPQLYDFTETHNQGRPICIA TDDYESE-----SG---SMIS
HC5	LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT
HC2A	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQOSS
KIAA	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQOSS
rat	-----
HC4	TDKDTAYGSFQNG-----HGIKREDSRGS LIP-EGATGFDPQNGTGEN-----TRQS
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLSDSNPSTNEKSSEKTDNCEKIPRPL
HC3	QTVAMAIAGTSVPQ-----LTPGSGFLLTSTSGRQHT
HC5	QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----

FIG. 5A (cont.)

HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDDFFTISEVCL
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDDFFTISEVCL
rat	-----
HC4	STRSSVSQYNRLDQYEIRSLIMCYLYIVKMI SEDTLLTYWN-KVSPQELINILILLEVCL
HC1	ALIGSTLRFDRLDQAE TRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLDLLLYLCV
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV
HC2A	HQFQYMCKRYIARNQEGLG--PIVHDRKS-----QTFVSRNRTGMM
KIAA	HQFQYMCKRYIAR-----TGMM
rat	-----
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNSGVM
HC1	QNFYLGKRNIIRKIAAAF--KFVQSTQNNGTILKGSNPSCQTSGLLAQWMHSTSRHEGHK
HC3	SCFEYKGKKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
HC5	LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGE GARGEMM
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1	QHRSTLPIIRGK---NALSNPKL---LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC
HC3	RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAEILDQEALISGNLATEAH
HC2A	LTALDTLSLFTLAFKNQLLADHGHNPIMKKVFDVYLCFLQKHQSE TALKNVFTALRS LIY
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPIMKKVFDVYLCFLQKHQSE TALKNVFTALRS LIY
rat	-----KLSRGHSPIMKKVFDVYLCFLQKHQSE MALKNVFTALRS LIY
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVF DIHLAFLKNGQSEVSLKHVFASIRAFIS
HC1	LTILDVLSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVNSATALKHVFASIRLRFVC
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLKVLHSMACNQSAVYLQHC FATQRALVS
HC5	LIILDMQENIQASS--ALDC--KDSLLGGVLRVLVNSLNC DQSTTYLTHCFATLRALIA
HC2A	KFPSTFYEGRADMC AALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
KIAA	KFPSTFYEGRADMC AALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
HC4	KFPSAFFKGRVNMCAAFCEYVLKCCTSKISSSTRNEASALLYLIMRNNFEYTKRKTFLRTH
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3	KFPELLFEEETEQCADLCRLRLRHCS SIGTIRSHPSASLYLLMRQNF EIGN--NFARVK
HC5	KFGDLLFEEVEQC FDLCHQVLHHCSSSMDVTRSQCATLYLLMRFSFGATS--NFARVK
HC2A	LQVII SVS QLIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM
KIAA	LQVII SVS QLIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM
rat	LQVII SLSQLIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM
HC4	LQIIIAVS QLIADVALSGGSRFQESLFI INNFANS DRPMLARAFPAE VKDLTKRIRTVLM
HC1	LQLIKAVS QLIAD-AGIGGSRFQHS LAITNNFANGDKQMKNSNFP AEVKDLTKRIRTVLM
HC3	MQVPMSLSSIVGTSQNFNEEFLRRSLK TILTYAEEDLELRETTFPDQVDLVFNLMHLS
HC5	MQVTMSLASIVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMT PFPPTQVEELLCNLNSILY

FIG. 5A (cont.)

Transmembrane

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN	DLSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN	DLSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN	DLSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD SMAKIHVKN	DFSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLE SMAKIHARNG	DLSEAAMCYIHI
HC3	DTVQMKEHQEDPEMLIDLMYRIAKGYQTS PDLRLTWLQNMAGKHSERSN	HAEAAQCLVHS
HC5	DTVQMREFQEDPEMLMDIMYRIAKSYQAS PDLRLTWLQNMAEKHTKKKCY	TEAAMCLVHA

		SH3	
HC2A	TALVAEYI	TRKGV-----	FRQGCTAFRVITPN
KIAA	TALVAEYI	TRKEA-----	VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYI	TRKEAD-----	LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEFI	HRKKL-----	FPNGCSAFKKITPN
HC1	AALIAEYI	KRKGWYKVEKIC	TASLLSEDTHPCDNSNLLTTPSGGSMFSGMWPFLSITPN
HC3	AALVAEYI	SMLD-----	RKYLPGVCVTFQNISSN
HC5	AALVAEYI	SMLD-----	HSYLPVGSVSFQNISSN

HC2A	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIP
KIAA	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIP
rat	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4	IDEEGAMKEDAGMMD-----	VHYSEEVLLLELLEQCVNGLWKAERYEIISEISKLIGPI
HC1	IKKEGAAKEDSGMHD-----	TPYNENILVEQLYMCGEFLWKSEYELIADVKNPIIAV
HC3	VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASF	SMAGMYEAVNEVYKVLIP
HC5	VLEESVVSSEDTLSPDEGDGVCAGQYFTESGLVGLLEQAAELF	STGGLYETVNEVYKVLIP

		ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD-----				
KIAA	YEKRRD	FERLAHL	YDTL	HRAYS	SKVTEVMHSGRLLGTYFRVAF
rat	SMKSGGTLE	THLYDTL	HRPYS	SKVTEVITR-----	A-----AGSWDLLPGGLFGQ
HC4	YENRREFENL	TQVYRTL	HGAYT	KILEVMHTKKRLLG-----	TFRVAFYFGQ
HC1	FEKQRDFK	KLSDIYYD	IHRSYL	KVAEVVNSEKRLFG-----	RYRVAFYFGQ
HC3	HEANRDAK	KLSTIHGKL	QEA	FSKIVHQSTGWERMFG-----	TYFRVGFYFG-
HC5	LEAHREFR	KLTLTHSKL	QRA	FDSIVNKDH--KRMFG-----	TYFRVGFYFG-

		ITAM	ITAM
HC2A	-FFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFG	SENVKMIQDSGKVNPKDLD	SKYA
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFG	SENVKMIQDSGKVNPKDLD	SKYA
rat	GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFG	SENVKMIQDSGKVNPKDLD	SKFA
HC4	SFFEEEDGKEYIYKEPKLTGLSEISLRVLKLYGEKFG	TENVKIIQDSKVNKELDP	KYA
HC1	GFFEEEGKEYIYKEPKLTGLSEISQRLLKLYADKFG	ADNVKIIQDSNVKVNPKDLD	PKYA
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRLEGFYGER	FGEDVVEVIKDSNPVDKCKLD	PNKA
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGC	FGAEFVEVIKDSNPVDKCKLD	PNKA

	ITAM
HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQKRRRTILTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQKRRRTILTA
rat	YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVVEEQKRRRTILTA
HC4	HIQVTVVKPYFDDKELTERKTEFERNHNISRFVFEAPYTLGKKQGCIEEQKRRRTILT
HC1	YIQVTVVTPFFEEKEIEDRKTDFFEMHHNINRFVFETPFTLSGKKHGGVAEQKRRRTILT
HC3	YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGEHQFRRKTILT
HC5	YIQITFVEPYFDEYEMKDRVTFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLT

FIG. 5A (cont.)

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		<u>Coiled-Coil 1</u>
HC2A	IHC	FPYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELRQLC
KIAA	IAA	FPYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELRQLC
rat	rat	FPYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELRQLC
HC4	HC4	FPYVKKRIPINCEQQINIKPIDGATDEIKDKTAE
HC1	HC1	FPYVKKRIQVISQSSTEINPIEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV
HC3	HC3	FPYIKTRVNVTHKEEIIITPIEVAIDEMQKKTQELAFATHQDPADPKMLQMLVQGSV
HC5	HC5	FPYIKTRISVIQKEEFVITPIEVAIDEMKKKTLQLAVAINQEPDAKMLQMLVQGSV
		<u>Coiled-Coil 2</u>
HC2A	SVQVNAGPLAYARAF	LDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
KIAA	IAA	SVQVNAGPLAYARAF
rat	rat	SVQVNAGPLAYARAF
HC4	HC4	SVQVNAGPLAYARAF
HC1	HC1	SVQVNAGPLAYARAF
HC3	HC3	SVQVNAGPLAYARAF
HC5	HC5	SVQVNAGPLAYARAF
		<u>Coiled-Coil 2</u>
HC2A	YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPSTMTVHG	TSS
KIAA	IAA	YQEEMKANYREMAKELSEIMHEQLG-----
rat	rat	YQEEMKANYREIRKELSDIIVPRICPGEDKRATKFAHLQRHQ
HC4	HC4	YHEGLKSNFRDMVKELSDIIEHQILQEDTMHSPWMSNTLHVFC
HC1	HC1	YQEELRSHYKMDLSELSTVMNEQITGRDDLK---RGVDQCT
HC3	HC3	YQRELG---KLSS-----PZ-----
HC5	HC5	YQELKKNYNKLNENLRPMIERKIPELYKPIFRVESQKRD
		<u>PBM</u>
HC2A	SSVVZ-----	
KIAA	IAA	CVTLPHVPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWT
rat	rat	CVTLPHVPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWT
HC4	HC4	CVTLPHVPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWT
HC1	HC1	CVTLPHVPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWT
HC3	HC3	CVTLPHVPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWT
HC5	HC5	CVTLPHVPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWT
		<u>VHIF</u>
HC2A	-----	
KIAA	IAA	-----
rat	rat	VHIF
HC4	HC4	-----
HC1	HC1	-----
HC3	HC3	-----
HC5	HC5	-----

FIG. 5A (cont.)

	A	B	
CLASP-1	YRVAFYGQ::::::::::::GFFEEEEGKEYIYKEP		
KIAA1058	FRVAFFGQAAQYQFTDSETDVEGFFEDEDGKEYIYKEP		
CLASP-2		FEDEDGKEYIYKEP	
CLASP-6	FRVAFFGQ::::::::::::GFFEDEDGKEYIYKEP		
CLASP-4	FRVAFYGQ::::::::::::SFFEEDGKEYIYKEP		
DOCK180	FAVGYYGQ::::::::GFP TFLRGKVFIYRGKEYERRED		
DOCK2	FAVGYYGQ::::::::GFP SFLRNKVFIYRGKEYERRED		
DOCK3	FRVGFYGR::::::::::::KFPFFLRNKEYVCRGH		
KIAA0716	FRVGFYGR::::::::::::KFPFFLRNKEYVCRGH		
CLASP-3	FRVGFYGT::::::::::::KFGDLDEQEFVYKEP		
CONSENSUS	F V FYG YF	KEY K Q F R	
			C
TRG	<u>PKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKEFYIQVTHVTPFFDEKE</u>		
CLASP-1	PKLTGLSEISQRLCLKLYADKFGADNVKIIQDSNVNPKDLDPKYAYIQVTYVTPFFEEKE		
CLASP-2	PKLTPLSEISQRLCLKLYSDKFGSENVKMTQDSGKVNPKDLDSKYAYIQVTHVTPFFDEKE		
CLASP-4	PKLTGLSEISLRLVKLYGEKFGTENVKIIQDSKVNAKELDPKYAHIQVTYVTPFFDKE		
CLASP-3	PAITKLAIEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKAYIQITYVEPYFDTYE		
KIAA0716	H DYERLEAFQQRMLNEFPFAIA-----MQHANQPDETIFQAEAQYLQIYAVTPIPE SQE		
DOCK3	H DYERLEAFQQRMLSEFPQAVA-----MQHPNHPDDAILQCDAAQYLQIYAVTPIPDYVD		
DOCK2	FQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPGOYIQCFTVQPVLEHP		
DOCK180	EYERREDFQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPGOYIQCFTVQPVLEHP		
CONSENSUS	L L Y M F	YIQ+ V P D L E	
	D	E	
CLASP-1	RTILTTSHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELN		
TRG	RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELH		
KIAA1058	RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR		
CLASP-2	RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR		
CLASP-6	RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEV:HDEM SKKVAELR		
CLASP-4	RTILTTSNSFPYVKKRIPINCEQQINLKPIDVATDEIKDKTAELO		
CLASP-3	KTILTTSHAFPIYIKTRVNVTHKEEIIILPIEVAIEDMOKKTQELA		
CLASP-5	NTVLTTMHAFPIYIKTRISVIQKEEFVLTPIEVAIEDMOKKTLQLA		
KIAA0716	RTSLYLVSPLPGISRWFVEVEKREVVMSPLENAIEVLENKNQQLK		
DOCK2	RTSFVTAYKLPGLRWFEVVHMSQTTISPLENAIETMSTANEKIL		
DOCK3	RTTLTLTHSLPGISRWFVEVERRELVEVSPLENAIQVVENKNQELR		
DOCK180	RTSFVTAYKLPGLRWFEVVHMSQTTISPLENAIETMSTANEKIL		
CONSENSUS	RT L FP V + V + P+E AI+ M +L F L L + I		

FIG. 5B

	F				G															
CLASP-1	SLQLKLQGSVSVKVNAG				PMAYARAFLEETNAKKY				PDNQV--KLLKEIFRQFADACGQALD											
TRG	KLQLKLQGSVSVQVNAG				PLAYARAF				LDDTNTKRYEDNKV--KILKEVFRQFVEACGQALA											
KIAA1058	KLQLKLQGSVSVQVNAG				PLAYARAF				LDDTNTKRYEDNKV--KILKEVFRQFVEACGQALA											
CLASP-2	KLQLKLQGSVSVQVNAG				PLAYARAF				LDDTNTKRYEDNKV--KILKEVFRQFVEACGQALA											
CLASP-6	KLQLKLQGSVSVQVNAG				PLAYARAF				LDDTNTKRYEDNKV--KILKEVFRQFVEACGQALA											
CLASP-3	MLQMVLQGSVGT				TVNQGLEVAQVFLSE--IPSD				EKLFRHHNKLRLCFKDF				TKRCEDALR							
CLASP-4	QLQLKLQGC				SVQVNAGPLAYARAF				LND				SQASKY	P	PKVSELKDMFRKFI--QAC	SI	ALE			
CLASP-5	MLQMVLQGSV				GATVNGGLEVAQVFLAE--IPAD				EKLFRHHNKLRLCFKEF				FIMRCGEAVE							
KIAA0716	PLTMCLNGVIDA				AVNGGVSRYQE				AFFVKEYILSH				EDGEK				IARL	RELMLEQAQILEF	GLA	
DOCK2	PLSMLLNGIVD				PAVMGGFAKYE				KAFFTEEYVRD				HE				DQDKLTHL	KDLIAWQIPFL	GAGIK	
DOCK3	LLSMCLNGVIDA				AVNGGIARYQE				AFDDKYINKH				EGDAEKITQLKELM				QEQVHVLGVGLA			
DOCK180	PLSMLLNGIVD				PAVMGGFAKYE				KAFFTEEYVRD				HEAHEKIEKL				KDLIAWQIPFL	AEGIR		
CONSENSUS	L M L+G V VN G				Y AFL + + E				L+				L							
	L I				V V F +								I							

DOCK2=KIAA0209

DOCK3=KIAA0299

CLASP2variant=KIAA1058

FIG. 5B (cont.)

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1
A

2 32
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr


62 92
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122 152
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr
ref 1.1, 1.2 and 1.3

362 392
GTG TAT ACT CAG  GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 6A

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722	752
ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA	
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser	
782	812
TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA	
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys	
842	Cadherin Cleavage 872
GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT	
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val	
902	932
GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG	
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys	
962	992
AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC	
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly	
	ref 2.1
1022	1052
TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC	
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr	
1082	1112
CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG	
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro	
1142	1172
TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT	
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu	
1202	1232
GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG	
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg	
1262	1292
GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC	
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu	
	ref 3.1
1322	1352
AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA	
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala	
1382	1412/471
AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC	
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile	
1442	1472
AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC	
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser	

FIG. 6A (cont.)

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1502
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn
ref 4.1 and 4.2

1562
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1622
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp
ref 5.1 and 5.2

1682
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1742
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1802
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1862
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val
ref 6.1

1922
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1982
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2042
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2102
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala
ref 7.1

2162
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

2222
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

2282
2312

FIG. 6A (cont.)

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TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342 2372
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402 2432
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462 2492
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522 2552
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582 2612
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642 2672
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702 2732
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762 2792
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822 2852 |XXXXXXXXXXXXXXXXXXXX Predicted
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

Transmembrane Domain XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX|
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942 2972
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu

ref 8.1 ↓

3002 3032
GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG
asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062 3092
TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT
cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

FIG. 6A (cont.)

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                                ref 9.1
3122                               3152
ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT
ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

3182                               3212
ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG
ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu
                                ref 10.1
3242                               3272
TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC
tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

3302                               3332
CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT
pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3362                               3392
GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC
asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

3422                               3452
TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG
phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln
                                ref 11.1
3482                               3512
TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC
cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys lys arg ile

3542                               3572 |xxxxxxxxx Coiled-coil 1 xxxxxxxx
CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG
pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

3602 xxxxxxxx Coiled coil 1 cont'd xxx 3632 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA
ser lys lys val ala glu leu arg gln leu cys ser ala glu val asp met ile lys
                                ref 12.1
3662 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx | 3692
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3722                               3752
GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG
ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

3782                               3812 |xxxxxxxxxxxxxxxxxxxxxxxxxxxx
CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu

3842 xxxxxxxx Coiled coil 2 xxxxxxxxxxxx 3872 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA
arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

3902 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx 3932 xxx|

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FIG. 6A (cont.)

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ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962 3992
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022 |xxxxx PBM xxxxxx|
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG
met val his gly met thr ser ser ser val val STP

4082 4112
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142 4172
ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202 4232
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262 4292
GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322 4352
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382 4412
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

4442 ref 13.1 4472
CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502 4532
GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562 4592
TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT

4622 4652 ref 14.1
GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682 4712
TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742 4772
ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802
TTT ACT

FIG. 6A (cont.)

BAC sequences of Human CLASP 2

Ref 1.1

Sequence of BAC4 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is underlined and represents nucleotides 356-375.

TTTCTACAGNGTNTACTCAGGTATGTGCTCCTTCAACAAAATTAGCAGTTGCTGCTCT
 GTGACAAAGTTTGCACCATTTTGCAGAAGAAAAAATCCTAATGTGTTATATTACTA
 TATTTTACTCTATAGATCTTTTTCTAAAGAAAGAAAGTACAAGTGAAGTGCTTATAT
 GTATTCATATAAATGACTAGTACAAGCATCATTTTGCACAGATTTCCTTTCATTG
 GAGGATCTTCTTGATGTTATTTGTACACGATCAATTTTGTAGTCTTAATAAGATGAGGC
 TGGGTGTGGTGGCTCACACCTGTAATCCTAGCATTTTGGAGGCCAAGGTGGGCAGAT
 CACTTTAGCCCAGGGGTTTGAGACCAGCCTGGCCAACATGGCAAAACCTTGTCTCTA
 CAAAAATACNAAAATTATCCAGGCATGGTGATGTGTGCCTGTAGTCCCAACTNCTAG
 GAGGCTAGGGGTAGGGGGATTGCAAGAGGCTGGGAGGGTCAAAGCCCNAANTGAG
 CCATTGGTNCATGTCACTTGGACCCCAAGCNGGGGNGANCAAGAGCAAAGGACTNN
 TGTNNTTTANAAAAAAAACCGGGCTACCATAACNACCAACCCNCNACCTACCCNACC
 TTTCCANNTTAAAAANAAGGCTTTGNCTTGCANAGGAAAAANCAAAATNNCC

Ref 1.2

Sequence of BAC26 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is underlined and represents nucleotides 351-375.

TCTGGTTTCTACAGTGTATACTNAGGTATGTGCTCCTTNAACAAAATTAGCAGTTGCT
 GCTCTGTGACAAAGTTTGCACCATTTTGCAGAAGAAAAAATCCTAATGTGTTATAT
 TACTATATTTTTACTCTATAGATCTTTTTCTAAAGAAAGAAAGTACAAGTGAAGTGCTT
 ATATGTATTCATATAAATGACTAGTACAAGCATCATTTTGCACAGATTTCCTTTC
 ATTGGAGGATCTTCTTGATGTTATTTGTACACGATCAATTTTGTAGTCTTAATAAGATG
 AGGCTGGGTGTGGTGGCTCACACCTGTAATCCTAGCATTTTGGAGGCCAAGGTGGGC
 AGATCACTTTAGCCCAGGGGTTTGAGACCAGCCTGGCCAACATGGCAAAACCTTGTCT
 TCTACAAAAATACAAAAATTATCCAGGCATGGTGATGTGTGCCTGTAGTCCCAGCTAC
 CTAGGAGGCTAGGGTAGGGGGATTGCAAGAGGCTNGGAGGTCAAAGGCCGAGTGA
 GCCATGGTCATGTCACTGCACCCCAAGCCAGGGCCGACAGGAGCAAGACTNNTGTNT
 CAAAAAAAACAGNAACCAACANCCAACAACAACNACCTTTCNGCAAAAANAAGC
 TTGCTNCAANGAAACCAAAATGNCTTCTTNTTTTCCCCCN

Ref 1.3

Sequence of BAC26 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is not found within this sequence. This sequence most likely represent intron sequence since this sequence matches the intron sequence found in the previous two BAC sequences.

AGNNNNNCCCNCTACNCCACTTTTAACCTTTTGAAAAACACAGTGTNNCTCAANTATG
 CGCTCCTTCACATATTAGCAGTTGCTCTGTGACATAGTTGCACCATTNTGCAAGA
 AGAAAAAATCCTAAGTGTNATATCACTATATNNNTACTCTATAGATCTTNTCTAAAGA
 AAGAAAGTCAACTGATGTGCTTATATGTATNCATATAAATGACTAGTACATGCATCAT
 TTTGCAACAGATNTCTCCTCACATTGGAGGATCTTCTNGANGNATTCGACACGATNAN
 TATTAGTCTNAATAAGATGANGCTGGTGTGGNGGTACACTGNATCTAGCATNTGGAN
 GCATGTGGCAGACACTTANCCNCGGTNGAGACAGCTGTCACTGNCNAACTGTCTCTN
 TAAANCAAANNCTCCGCNGGNGATGGGCTGAGCCAGTCCTAGNNGCTAGNTAGNGAT

FIG. 6A (cont.)

GNNGAGNTGTNGCACGNCGAGNGAGCATGNTCTGTACTGACTCATCAGGCGNCNACA
 CGNTCTGTTCNAAAAACATACCACACACACTCNCACCTNCGCAAAATTGCTCTNNAAAN
 ATGCTTNTTTCACACNGNTNCAATCNCCTATATNNTCTTCTATTCTNCNACGTNTNATTA
 NNATCTTNCNCTGCANAAACNATNCGNCCACCTNNANNACCTTANGCTTNGTTTCACGC
 TTATAGCTCCCCTACACNTNNCAGCNNTTNCNNGTGAAGGGCCNCCCGAATCTACGA
 NCATACTCTCTCCGTATATNGCCTCGGTCANCGCCATCTGCTGTNTNCTCNCNTNG
 CNNTTNANCNGTNCGCTATCTCTNNNCCGGATCCNCCATATNNTNNTCTACTTAN
 AGCGTAANNTNTNCNCNCACTANTCACAACCTTNTNNTNNAACTCTATCTNCTCCTCT
 CTACCACCTCACTTACTACCTNTTCAACNANTCTCCTTCNCTNTCCACTGATCTCCACA
 TAGCTGCTNTACTCGCCANTTTATCATATNCACACNCTCTACGCTNNNTNT

Ref 2.1

Sequence of BAC4 using primer HC2S1, which spans nucleotides 1107-1126 of the cDNA. Exon sequence is underlined and represents nucleotides 1079-1097.

CTTGATTNAAAGAGGGTCTGCAGGAAGAAGTGTGTAGTCATAAATACCTCACTGGA
 TATTTTATACAGGATTCTAAAAACCTATTAGCAATAGTATGCTAGAAATAGTCATTA
 GCTTCTTGACCTTCTTAGAACTGCACACTCTATTGCACTGTACAGATTTCAGGATGGC
 TGCAGGGATTGATTTGAAAACTAAGGACACATTTCAATAAACAATGTCTTCAATTGAT
 TTTTAGGGCTCCTCCTACTTCAATGAAGGACTTCAGGTAGCTTATAATTACAGACACA
 GGCTCAATACAATAAAAAAATTAGTAAGGCAGAGCTTTAAAAAAGGAAAAA
 GATAATTCTACCAGAGAAAGGCTACATGGTGACTTCTGTTACCAGTAACAACCCCG
 CACTACCTTTGGGTCTCCAGGAGCAAAACAGCTAATGTAGTTGTTGATCTGCTTGAAG
 ACAAGCCCCTGTCCATGAAGGTGAAACATCTCTGTGGAGGAAAACAAGCAAAAAAG
 TTATTTCAAGGTCCAAACATTTTCGGAAATTTGGATTCAAAGCAGGCATTTATTGCTAAT
 AAGTTTATCCACTGACATAAAAAACATGCCTTCAACATTGCCAGAGCACCTACTCTAT
 TNTAGTCNCN

Ref 3.1

Sequence of BAC4 using primer C96AS, which spans nucleotides 1443-1452 of the cDNA. Exon sequence is underlined and represents nucleotides 1370-1422.

AATCAGCAGACCAAACAGAGGCAGGTAGAGGGTGGCTATCCTTGCCTGATGGCTCTG
 AAAAGAAGACACACATGGTAAGTTTGACCCAGGATTCTGAGAACCGAACATAAGTTGG
 TGCTGACCATCTCCTTTATTTGGATCCTTCCTATAAAGACAGATATTTGATTTTAGTCC
 CAAAATAGAGCAAAATCTTAGTGCTGTTACCATGAATTTTCTAACTGATTACTTTCTTT
 ACACCACTTAAAATAAAGGACATTATCAATGCACATTCCTTCCATTGGGGACCACTCA
 CCCTTGAAGCATATCTGTTCATCAAAAGAATGCTTTATCAGCAGGTTCTTGAGCACACT
 GATGGCGATCAGACGGACCTCCCGGAACCTCCTGGAGGGCTGTCCCCACCTCCCTNAG
 TAACAGTCCCACCAAGAAGTGGTTTCTGCAGAACTCATCTGTTAATGAGTAGTCAAGC
 TGGGAGGTCTGAAATGAGGATAGAACTACTTTGNGTTAGGAAAGATGCAATGCTCT
 TTTGAATAAAACAAACAAACCAAAACNAACAAAAAAGATGCAATGCTCT
 ATTTCAAGCCCACCCTGGGGTNGGTCAAAGAGATGATCAGNANTTTGGCNTTNAAT
 GAAGAAAGAAATNAATTNTCCAGGGGNTGTTCTNCTTTTAGCACANGGAGGGATNT
 TAANTGAAAACCAATTTAAATCCAATTNAGGNG

FIG. 6A (cont.)

Ref 4.1

Sequence of BAC4 using primer C2AS5, which spans nucleotides 1716-1735 of the cDNA. Exon sequence is underlined and represents nucleotides 1602-1703.

TTCCTTTCTGCAAGGCTGTTCCCGAATCTGTGCTTATGAGAGATCCTCTCGAATCAGC
ATTTCTCACACTGTTGATGTTTGGAGTTGAGGTTGTATATGGAGAAGCTAAATGGAAA
 TCAAGCCAACAATAAAGTTTTATTAAGACAGAACAAAATAAAGATGAGTACTGAACTT
 TAAGGGAAATTGCTTTTATTGCACTTATTTTTTCTGTTAGGAAGTTGGCTCAAGAGTT
 GCATTCCATTACTTCACCTTTAAAGAACCAGGTCATATACAATGAGATAAAAAAGAAAC
 TAGTCTGAAACATTCAGATGTAAACATCAATTCACTTGTTAGAAACCACCTTTGATCG
 CTAAAGACTAAATGCATACCTGTTTCAGAATGTGATAGAATGAAGACTTAAAAAAATT
 AAAAGATAAAATCCACCTACAACATATCAAATCACAAAATTAAACCACACAACAACTTG
 TAGCATTCAAACCTGGTAATAAACACTGAGGAGCCTACCCAACTCTGAGGGGTGTCAT
 GGGGTATTTTAAATTTTCGAGGAGAACACAGTGATATGTGACCTCAGCCAGAAGCTG
 CTGTTTNAGCAGGTTGGTGCTATGCTCCTTTTTGAAGACATATTTGTGAAGCTGG
 GTATTTTGGGGGGCCTGCTTATGATAAAAANGGCAAGGTNTTCAATGNAGGGGN

Ref 4.2

Sequence of BAC26 using primer C2AS5, which spans nucleotides 1716-1735 of the cDNA. Exon sequence is underlined and represents nucleotides 1602-1703.

TTCCTTTCTGGAAGGCTGTTACCCGAATCTGTGCTTATGAGAGATCCTCTCGAATCAG
CATTTCTCACACTGTTGATGTTTGGAGTTGAGGTTGTATATGGAGAAGCTAAATGGAA
 ATCAAGCCAACAATAAAGTTTTATTAAGACAGAACAAAATAAAGATGAGTACTGAACT
 TTAAGGGAAATTGCTTTTATTGCACTTATTTTTTCTGTTAGGAAGTTGGCTCAAGAGT
 TGCATTCCATTACTTCACCTTTAAAGAACCAGGTCATATACAATGAGATAAAAAAGAA
 CTAGTCTGAAACATTCAGATGTAAACATCAATTCACTTGTTAGAAACCACCTTTGATC
 GCTAAAGACTAAATGCATACCTGTTTCAGAATGTGATAGAATGAAGACTTAAAAAAAT
 TAAAAGATAAAATCCACCTACAACATATCAAATCACAAAATTAAACCNCACAACAACTT
 GTAGCATTCAAACCTGGTAATAAAAACACTGAGGAGCCTACCCAACTTTGAGGGGTGTC
 AATGGGGTNTTTTTAAATTTTTCGNGGGANANCCAGTGNTATGGTGACCTTCACCCA
 AGAAGCTTGTTTGTNNACCAAGCNAAGGTTGNCTNTGCTCCTTTTTAGAAANACNNTA
 TTTTNNNAAATNCTGGNTTTTTTNNNGGCCCCCTNCNTTNT

Ref 5.1

Sequence of BAC4 using primer C2S6, which spans nucleotides 1686-1705 of the cDNA. Exon sequence is underlined and represents nucleotides 1724-1736.

TTCCTGGATAAGGTAATTGCTTTTACCCAACACAAATGTTTCTTATAATCAATGGATT
TAGCCCAAAGTAAACGTAATTCATGTTCTAGTGCTTTTAAAGTGTGACCTTTTGTTTT
TTTCTAAACCACCCGGCTGACCTGGAGTAGGTGATGAGAGCTTTAAGGTTGGGGCCC
ATTCCTTGAAGTGCTCTGATTCTGTTTCCAGTACCTCAGATCCTGGGCAGGGTTTGC
AGTGGAGCGTCTTGAGTGAATGGCTCTGGTGGGTTGAACGGGGAGGGACTCAAAAT
GCTGCCCATCTCAATTTCTGTAGTCTTTTTATTTATTTATTTTATTTTGGACAGAG
TCTCGCTCTGTGCCCCAGGCTGGAGTACAGCGGCACGATCTCAATTNACTGCAACCT
CCGCCTCC: TGGGTTCAAACGACTCCTCTGCCTCAGCCTCCCCAGCAGC: TGGGACCA
CAGGCACAAGCCACCACCGCCCGGCTAATTTTTGTNTTTTAGTA: GAGAT: GGGGTT
TCACCATATTTGGCCAGGCTGGGCTCAAACCTCCTGACC: TCGTCATCCGCNCCCTCGG
NCTNCCAAAGTGCTTGGGATTNCAGGCNGTGAGCCCACTTACACCTNGGGCAATTCC
CTGTNAGTCTTTTTTACCAGAGACACCATCATTCAACACAGCTTTTCCACCCACAA

FIG. 6A (cont.)

Ref 5.2

Sequence of BAC26 using primer C2S6, which spans nucleotides 1686-1705 of the cDNA. Exon sequence is underlined and represents nucleotides 1712-1736.

TGAGAAGAGCAATTTCTGGATAAGGTAATTGCTTTTACCCAACACAAATGTTTCTTA
 TAATCAATGGATTTAGCCCAAAGTAAACGTACTTCATGTTCTAGTGCCTTTTAAGTGT
 GACCTTTTGTTTTTTTCTAAACCACCCGGCTGACCTGGAGTAGGTGATGAGAGCTTTA
 AGGTTGGGGCCCATTCCTTGAAGTGCTCTGATTCCTGTTTCCAGTACCTCAGATCCTG
 GGCAGGGTTTGCAGTGGAGCGTCTTGAGTGAATGGCTCTGGTGGGTGAACGGGGA
 GGGACTCAAAATGCTGCCCATCTCAATTTCTGTAGTCTTTTTATTTATTTATTTATTT
 TTTGAGACAGAGTCTCGCTCTGTGCGCCAGGCTGGAGTACAGCGGCACGATCTCAAT
 TCACTGCAACCTCCGNCCTCCCTGGGTTCAAACGACTCCTCTGNCTNAGNCTCCC:AGC
 AGCCTGGGAACACAGGCTCANGCCACCACGCCCGGCTAATTNTTGAATTTTNAGT
 AANAAATTGGGGGTTCTCACCAINTTGGCCCAAGNCTTGGGCCTAAAAACCTTNCTNA
 CCNTCGNCATTNCNCCCCNACCNTGGGCNCTNCTCAAANGNGCTTGGGGATTANC
 ANNCGCNTTAACCCCCCNTATCACCGTGGNCCTTAATT

Ref 6.1

Sequence of BAC4 using primer C2S7, which spans nucleotides 1918-1937 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S7 is intron sequence.

NAGNGNGGGTTTNAGNCGTTTGAAGCCTGNNACGNGGTGNGTGCTNGAACTCTGTGG
 GCTTTCAGGTACTGGGGTATCTGGGAGCCTGCTGTTTGCATTGCTAGTGCATCAGAC
 CAGGGCTTTTCTCCCTGTAGCTGCTACTTATACACATAGCTCTAACTGAGATGATT
 CTCCAGACAACTGATGCAGAGCAGCAAAAGCTTCTGCCGTTCTCCCTTCTAGGAGT
 GTCTCCTTTCTTTGGAAAGAGATCATGAGGGGCTAGATTGTAATGAAGTGAGGCTCA
 GTGCTTGAGCACATCCGGTAAAAGTTCCAATATATTGGTCATAAAGTTTCTCATTCTT
 TATAGCAGTTAATTTCTCTGGCTCATGAGTTTTCTTAGTTTTAATCTGACTTTTAAATT
 AATGTCTCCAGCACCAGTCATATCCCCAGGGCAAACCTCAAAGGCATGAGAGGCCAGA
 CTCGGGTCCCTGGTCATAGCAACCCCTGTCTAGGGCCTTGGTCCCTGCCTCCGCTTGT
 GTGCTGTGGCGCAGGTCCTATGGGCCCTTAGGAAACAGGACCACCCTGTCGCACCCC
 CTACAGAGACCAGCCAAGTTTGACATTAGATCACCGTAGCAATGTNTGCAAATTCCA
 GTTCTTGCTAAAACAGGTTAAGCCTTGCAGCCACTTTATCTGTAAGTGGCNGAGGTT
 TTGACATAAAA

Ref 7.1

Sequence of BAC4 using primer C2S8, which spans nucleotides 2143-2162 of the cDNA. Exon sequence is underlined and represents nucleotides 2182-2219.

CTCTCGACACGCTGTTTCTATTAACATTGGCGTTTAAGGTTTGTATCAATTTGCTGTT
 CGNGGTTCTAGTTTTACCTTTCACATTCATTCTGCTTGGTAAGCTCAGTGAGCACAAA
 CTTACTATGTTGCATTTTTACTTCAGCAATTATTTTTGTCCCTGTAAGGAAACCATTAA
 TCTTTAAATTCCTTTAATGAAATCATTCCACAGTGAATGGCTTGAATGCCCTGAAATA
 AAATTTAACTGGTCAGTGTGTGCTGCGCGCTTGGGTATGGTGGAACACGGTCTCTG
 GAGGCAGTTAACTCTTGGCTCGAACCTTGAGGATGGTGAATATAGGCACCTAATCAG

FIG. 6A (cont.)

GCATTTCTGCCTTGAATATCTTTAAATATATCCAAATGTTATAGCGTTTAATTAGATT
 TTATGTAGAAAGGAGCAATAAACACAAGACACATGTTTTTCAGTTTTTTATCTGTTACT
 GCATTAAATGATAAAAACGTTTTGGAGATAGAAAATGAAAGGGGTTTTTTTTGTCT
 TGTTTTAAAGTTTTAGCAAATAATATCAAGTAGGTGGAGATGGACTCTTCACCACTC
 TCCTGTTTTTAGGAACCAATACTTTTTTCATTCTTGCTAAATGATTACTTCCATTCTA
 GCATAGAAAAGGAGAAAATTGGAATGAGTGTTTATAT

Ref 8.1

Sequence of BAC4 using primer C2S9, which spans nucleotides 2992-3011 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S9 is intron sequence

CGCTTTNAAATNCCAGCCGCTACTGCGGGGCGNTNAATTCGAAACGTGTTGTTNTCT
 GTGATGCCTGGCTCTGATTGTGTGGGATTGGTCATCAGTGGCGGTTGGCAGNTGGGG
 TTCATGGAAGCGGCCATGGGGACTGATGGCAGGCCCTTGGATTGCCACCGCAGAGCC
 TGGCAGTGTCTTTGGTCTGCATTCCCTACCGGCGAAGTCTCATTTACCTCACGTGTTA
 TCTCTTGGAAGCATTCCCTTAGCGGGCTGTGTCTACCCTTCCATCCTCTCGTCCAAA
 CTCCCCCTCCTTCTCTGTTCTGTCTCCTTCCCATCCTCTTCTCCCCAGTTCTTCTCCT
 ATGTTCCCTCCTCAGTGGTCTTCTTCCCTCTGTTTGACTTTCCAAGGTCATTTTGACTG
 TTCCTGTCTCCAACTACAAAGATACTAAATCTCACCTAACCCTCTTCTTCTTTCTTA
 ATGAAAGAATGTTTTTCAGTCCATCCCAAATTTGTGTGGACTTCACAAACCTTCTCTAA
 AATGGAGCCTTTTCTCTTCCCTACTCTTGACTAGNTGGTAAACGCTCCATGTTCTTGGC
 CAGAACTCCCTGGTGAGTAGCGTCACTCCCACTTTCTGTGCAGAACCAAGCCTCCT
 AGAAAACCTCTTTGCANCTGAGTGGGTTGGGACACGCCCTTTNTTTGGG

Ref 9.1

Sequence of BAC4 using primer C2AS10, which spans nucleotides 3276-3295 of the cDNA. Exon sequence is underlined and represents nucleotides 3147-3234.

TTTANACCNATNTATCCGNGTCAGTTANAGGAGTCTCTGAGAAATTTCCGACAGCGGT
GTGAGTTTGGGTTCCCTTGTAATATACTCCTTTCCATCTTCATCTTCAAAGAATCCCT
 GTGACATAAAGCACAATTAGAGCTATCCCTGAACGTAAGCCCAGGGCTTACCACCTA
 GGAAGCGTTCTTTTATTACAAGGGGGGAAAAAAGGAATGGGTCTAAAAATCCAGCTG
 AAATGGGCTTTCTGAATGAGAAAGAAAATGCTAATAACATGAAGTCTAGGTGCAAAG
 GTAAAGGAAAAACACAACATTGCAAACTTATTCAAGAATGCAGTCATTAAGTGTTGAG
 TGAAATGAAAGATTTTGGATACAAGACTAAGCTGTCCCAGGGAAGTCTAATGGGAGT
 CAAGCCTGTTTCACTTTCCCAAGAAGCAGAACTCACTANAAAATGATGAGCAGCCCA
 CGACAGGCAGGCTCAGAAGTGGACATGCCTCCCTTCTCCTGATGGCTNCCATGCACA
 CAGGATTTTATGGCATGAACTGAAGCGTTTGGGGGTCTGGAGTAAGTTTAGTAAAAG
 TTAGGTAAAGCTTGTATAAATTGTATTTTGTCTTACCCGATGAGAAAAAAAATATTN
 AAGACCTGGTAGCTTCAATATTCAAGAAAAATATTTTTCATNTCACCCG

Ref 10.1

Sequence of BAC4 using primer C2S11, which spans nucleotides 3167-3186 of the cDNA. Exon sequence is underlined and represents nucleotides 3231-3296.

NGNANGTGGAGCCNCGANCCAGGGACAATCTNAACCTNCTTAAACTGTACTCGGATN
AATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGCAAGGTATTGACCATGTT
 TGGANAAGTTTCATAGCAATGTAATGTTGTGATNCGATTACATATNATATATTTTAA
 ATGTNTATAGAAAAAACACANGAAAAATATTAAGGATTGTTGGCCCGTGAGTGGCA
 GGTGTATNTTCTTNCTGATCCTTTAGNGCCTTCCATTACATGCNTGACATTAAAAAA
 NCTTTATCGCCTAATTTTTGAAACATCTAATTTTACAAAATAATTAACCGTNTGGCCAN
 GNATATTNTCATTTTTAGGNCCAGCTATTTAGAAACTCTGACANAAATGAGGGGCTGT
 GGCTTNCCTNCCCTNNACTTGNCCCTCTTTCNNGNATGTACCACATGAACCTTGNCNCT
 CTTTCNCTNACCGGGTGGCATGTTANAGGACAGGTTGAAACCNCANTNGGGCNGGA
 NTTNGGTNNAATTGGGACACAATGGTACNANGCTCTATNGGAATNGAACTCTCCCN
 ACNNCNGTGNCCNTGGGGAAAAATGNGNCNNATTCATTTTN

Ref 11.1

Sequence of BAC4 using primer C2S12, which spans nucleotides 3474-3493 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S9 is intron sequence

AGNANNGTTNNGCAGCTGCANNTCTGGACCCANAGGCCGCANGGGCACGAGCCNNG
 ACACGCTCGGCAAAGAGCTGTCCAGAGGGATTGAGAAGCTTCAGGACTGGAAGGGTC
 TTTCGAGCTCAGTTAGCCACCCCCACACCCATTTGAGTTTCACATTTATCTAGTGCTT
 CCTTTTGAATACTTGGGATGTTTTTCTGTTGATCTGTTGGCACTTCCTTCTCCACAA
 GACCAGAAGCTCATATCCAATCTAAGGTCACTTACCCTTCTGAGAATCTGATGAAAT
 GGCGTGCTTATGTGCCTAGATGCTTTTGCACACAGTCTAAGGTGACTTATGGACTCC
 AGGTCCAGCAGCCACACCCAGTCCTGGGTCTCCGCACAGGGAGGGACCCGTCTTCAC
 ACACCTGTCTCAGGTTCTAGCATTGGGCTGCTTCAGCGGTCTCAGGCTGTGAGTAA
 TGGGATGTGAGCTTGGATCGCCCCACGCTGTTGNCCCCCGGGGGGCTTGGCCAGCTG
 GCCACTNGAAATGCCTCCTTTTGGCCAGGAAAGCTCACTGCATTTCAATGGGGNTTN
 TCCACGAAGTTCANCTTTANGGG

Ref 12.1

Sequence of BAC4 using primer C2S13, which spans nucleotides 3645-3664 of the cDNA. Exon sequence is underlined and represents nucleotides 3683-3699.

AGNAAGGTNNCTCANTNAANNCAGCGTGAGNGTTCAGGTGAGCCAGGCACAGCAGGC
 CGGAGGGGCAGCAGGGGACGTCCTTGCCCCTGGGTGACTTGAGAGTCGTTTCCACTAA
 CAAGGTCTACTTGAGAGCCTCGGTTTACCAAGTGATCCCTGCTCCCTTCCCCCAACGT
 NTGTGACATTTCTCCTGATATCAGAGGGGGAGGAAACCTCATGATCCCTGCCCCCG
 CCCATGAGGACTGACTGTGGGGACAAAGAGCCAGATCTCATAGACTACCCTGATTT
 GTCAGTATTTGGGGGAATTCTGGGTGCCTGATTAGAAGCATCAAGACTCTTCTAAATNC
 AAAGAAGTGTGGAGAGCAGTAGATTTTCTATAAAACTGGTGTGTGCTGGTTTCTATGA
 AAATTGGATCCAAAAAAGTCCTTAAGTTTACCCTCTTAATGGNATCTTTTGATTAAT
 GGAATTCATTATTTTAATATAGCCCAATCAATCCAATTTTCTTTATTGGTAGCATTTT
 TATGTTCTCTTTAAAAAATCTTGGNCTACCTCCAAAATTTACAGATGTTCTCCTAG
 GGTTTCTCCTTTTGGTTCAAGCATCCATTCAANGTCTTGCAGTCCATTCTGGGG

FIG. 6A (cont.)

Ref 13.1

Sequence of BAC4 using primer C2S14, which spans nucleotides 4289-4308 of the cDNA. Exon sequence is underlined and represents nucleotides 4321-4448.

GACTTANATTTATTCTTCCTTGCAGAGTAGTGTTAGAATAGATGGCCTACAGAAAAAA
AAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGATGCCTGGGGGAC
CTTTGCGCTCGAGGCTGAGCTGGAAAATCTTGAAAATATTTTTTTTTTCCTGTGGCAC
 ATTCAGGTTGAATACAAGAACTATTTTTGTGACTATGTTTTTGATGACCTAAGGGAAC
 TGACCATTGTAATTTTTGTACCANTGAACCANGAGATTAAAGTGCTTTTATATTCATTT
 CCTTGCATTAAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAACTAGTCAA
 GCANTTTAGAACCAAAGGCCTATNTTNATAACCGCAACTATGCTNAAAAGNACAAAGT
 AGTACAGNATATTGNTATGTACATATCATTGGTAATACACNCCNGGCNTTCTGTACA
 TATATGTATTACATTTCTACNTTTTAATACTCCCNTGGGCTTATGCCNTTAAGGTTAA
 NTTGNGATAAATTTNGGCTGTTCCNGTNTATNCNATACNCTTTT

Ref 14.1

Sequence of BAC4 using primer C2AS15, which spans nucleotides 4680-4700 of the cDNA. Exon sequence is underlined and represents nucleotides 4660-4683.

ATGAGAATGTAATACATATATGTACAGAATGCCAGGACTGTATTAACAATGATATGTA
 CATAACAATATACTGTACTACTTTGTACTTTTCAGCATAGTTGCGGTTATTAATATAG
 GCCTTTGGTTCTAAACTGCTTGACTAGTTTTAAGCTCACATAATTCCTTAAGCTTTCAT
 ATTTTCTTAAATGCAAGGAAATGAATATAAAAGCACTAAATCTCCTGGTTCAGTGGTA
 CAAAAATTACAATGGTCAGTTCCTTAGGTCATCAAAAAGTACACAAAAATAGTTC
 TTGTATTCAACCTGAATGTGCCACAGGAAAAAAAAAATATTTTCAAGATTTTCCAGCT
 CAGCCTCGAGGCAAAAGGCCCCAGGCATCAATGTCAGNGCAGCCCTCCTGCCATGT
 AGATCCCAGAACCTTTTTTTTTCTGTAGGCCATCTATTCTAACACTACTCTGCAGGGAG
 AATAAAATCTAAAGNCCAGCTCAAGAGTGCTACCACACCTTTGTTAAGACACAATGAA
 AACTTTGGATATTGGCAGGNGAGATTTAAAAAAAATGTGCCCTTTCTTACCACTCCT
 ATAGNAAAGTCTGGTTAAGAAATAACCGTTGGTCTTTATTTTCCTTTTNTTTCCCTTC
 CCTTGGGNCTTCCTGGGGCTCGG

FIG. 6A (cont.)

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HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTSAFAAVLHHHQNPEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNEFFQYC
KIAA	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNEFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLEKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

FIG. 6B

HC2A	IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSTN	
KIAA	IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSTN	
rat	-----	
HC4	LFHIVSKCHEEGLD SYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN	
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK	
HC3	TQAMDRSCNRMSSHTETSSFLQTLTGRLP---TKKLFHEELALQWVVCSG--SVR---E	
HC5	-----	
	Cadherin Cleavage	
HC2A	KLLRYSWFFFDVLIKSMQHLIENSKVKLI ¹ RNRQFFPASYHHAAETVVMMLMPHITQKFGD	
KIAA	KLLKYSWFFFDVLIKSMQHLIENSKVKLI ¹ RNRQFFPASYHHAAETVVMMLMPHITQKFRD	
rat	-----	
HC4	KLLKYSWFFFEIIAKSMATYLLEENKIKLTHGQRFPPKAYHHALHSLFLAIT-IVESQYAE	6.1
HC1	HVLKHSWFFFAIILKSMQHLIDTNKIQLRPPQRFPEYQNELDNLMVLSDHVITWKYKD	1.2/1.2/2.1/2
HC3	SALQQAWFFFEILMYKSMVHHLYFNDKLEARKSRFFPERFMDIDIAALVSTIASDIVSRFQK	
HC5	-----	
HC2A	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL	2.1
KIAA	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL	
rat	-----	
HC4	IPKESRNVNYSLASFLKCCLTMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL	7.1
HC1	ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQYKFDL	3.1/3.2
HC3	DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLDFL	
HC5	-----	
HC2A	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF	
KIAA	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF	
rat	-----	
HC4	QTICNHEHYIPLNLPM-----AFAKPKLQR-----VQDSNL----EYSLSDEY	
HC1	QEVQCQHEHFIPCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF	4.1/4.2
HC3	RIICSHHYVTLNLPCSLTPPASPSVSSATSSQSSGFSTNVQDQKIANMFELS--VPF	
HC5	-----MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA	
HC2A	CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT	3.1
KIAA	CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT	
rat	-----	
HC4	CKHHFLVGLLLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQ	8.1
HC1	CRKHFLIGILLREVGFALQEDQD----VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS	
HC3	RQOHYLAGLVLTAVILDPAEGLFGLHKKVINMVHNLSSHDSDPRYSDPQIKARVAM	
HC5	SSTS-SPGLLFTLAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVIAA	
HC2A	LYLPLFGLLLIENVQRINVRDVSPFPVNAG-MTVKDESALPAVNPLVTPQKGSTLDNSLH	
KIAA	LYLPLFGLLLIENVQRINVRDVSPFPVNAG-MTVKDESALPAVNPLVTPQKGSTLDNSLH	
rat	-----	
HC4	LYLPLFVGLLLIENIQRIAGRTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS	9.1
HC1	LYMPLYGMLLDNMPRIYLDLYPFTVNTSNQSSRDDLTNGGFQSQTAIKHANSVDTSFS	
HC3	LYLPLIGIIMETVPQLYDFTETHNQGRPICIAATDDYSE-----SG---SMIS	
HC5	LYLPLVGIILDALPQLCFTVADTRRYR---TSGSDEEQE-----GA---GAIT	
	4.1/4.2	
HC2A	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNLSPERNSEKSNSLDKHQOSS	5.1/5.2
KIAA	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNLSPERNSEKSNSLDKHQOSS	
rat	-----	
HC4	TDKDTAYGSFQNG-----HGKREDRSGSLIP-EGATGFPDQGNLTGEN-----TRQS	10.1
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL	3.1
HC3	QTVAMAIAGTSVPQ-----LTPRGSFLLTSTSGRQHT-----	2.1
HC5	QNALAIAGNNFN-----LKTSG-IVLSSSLPYKQYN-----	

FIG. 6B (cont.)

HC2A	TLGNSVVRCDKLDQSEIKSLIMCFLYILKSMSDDALFTYWN-KASTSEIMDFFTTISEVCL	
KIAA	TLGNSVVRCDKLDQSEIKSLIMCFLYILKSMSDDALFTYWN-KASTSEIMDFFTTISEVCL	
rat	-----	
HC4	STRSSVSQYNRLDQYEIRSLIMCYLYIVKMISEDLLTYWN-KVSPQELINILILLEVCL	
HC1	ALIGSTLRFDRLDQAETRSLIMCFHIMKTISYETLIAYWQ-RAPSPEVSDFFSIIIDVCL	11.1/11.2
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQNLRLDLLLYLCV	
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV	
HC2A	HQFQYMCKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM	6.1
KIAA	HQFQYMCKRYIAR-----TGMM	
rat	-----	
HC4	FHFRYMCKRNRIARVHDAWLSKHFGIDRS-----QTMPALRNRSQVM	
HC1	QNFRLGKRNIIRKIAAAF--KFVQSTQNNGLTKGSNPSCQTSGLLAQWMHSTSRHEGKH	
HC3	SCFEYKGKKVFERMNSLTFFK--KSKDMRAK-----LEEAILGSIGARQEMV	
HC5	LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEARGEMV	
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
rat	-----	
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS	
HC1	QHRSQTLPIIRGK---NALSNPKL---LQMLDNTMTSNSEIDIVHHVDTEANIATEGC	12.1/12.2
HC3	RRSRGQLERSPSGSAFGSQENLWRKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN	6.1/6.2
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH	
HC2A	LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSIIY	7.1
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSIIY	
rat	-----KL SRGHSPLMKKVFDVYLCFLQKHQSEALKNVFTALRSIIY	
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAEIS	
HC1	LTILDIVSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVQNQSATALKHVFASLRLFCV	13.1
HC3	LIILDLEIVVQTVS--VTES--KESILGGVLKVLHLSMACNQSAVYLQHCFAIQRALVS	
HC5	LIILDMQENIQASS--ALDC--KDSLLGGVLRVLVNSLNCQSTTYLTHCFATRLALIA	3.1
HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
rat	KFPSTFYEGRADMCASLCYEVILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
HC4	KFPSAFFKGRVNMCAAFCEVLKCCTSKISSRNEASALLYLFLMRNNFEYTKRKTFLRTH	
HC1	KFPSAFFQGPADLCGSFCYEVILKCCNHRSRSTQTEASALLYLFLMRKNFEFNKQKSIVRSH	
HC3	KFPPELLFEEETEQCADLCRLRLRHCCSSSIGTIRSHPSASLYLLMRQNFIGN--NFARVK	7.1/7.2
HC5	KFGDLLFEEVEEQCFDLCHQVLHHCSSSMDVTRSQCATLYLLMRFSFGATS--NFARVK	
HC2A	LQVVISVSQLIADVVGIGETRFFQQSLSIINNCCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
KIAA	LQVVISVSQLIADVVGIGETRFFQQSLSIINNCCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
rat	LQVVISLSQLIADVVGIGETRFFQQSLSIINNCCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
HC4	LQIIIAVSQLIADVALSGGSRFQESLFIINNCFANSRDRPMLARAFPAEVKDLTKRIRTVLM	
HC1	LQLIKAVSqliad-AGIGGSRFQHSLAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLM	14.1/14.2/15
HC3	MQVPMSSLSLVGTSQNFNEEFLRRSLKLTILTYAEEDLELRETTFPDQVQDLVFNLMILS	
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTFPTQVEELLCNLSILY	

FIG. 6B (cont.)

		Transmembrane	Ref.
HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAAMCYVHV		
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAAMCYVHV		
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAAMCYVHV		
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKRWLDSMAKIHVKNGDLSEAAMCYVHV		
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHI		16.1/16.2
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPLRLTWLQNMAGKHSERSNHAEAAQCCLVHS		
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQASPLRLTWLQNMAEKHTKKKCYTEAMCLVHA		
SH3			
HC2A	TALVAEYLTRKGV-----FRQGCTAFRVTITPN		
KIAA	TALVAEYLTRKEA-----VQWEPPLLPKSHSACLRRSRGGVFRQGCTAFRVTITPN		
rat	TALVAEYLTRKEAD-----LALQREPPVPFPYSHTSCQRKSRGGMFRQGCTAFRVTITPN		
HC4	AALVAEFLHRKKL-----FPNGCSAFKKITPN		
HC1	AALIAEYLKRGYWKVEKICTASLLSEDPHPCDSNSLLTTPSGGSMFSGWPAFLSITPN		
HC3	AALVAEYLSMLED-----RKYLPGVCVTFQNISSN		8.1/8.2
HC5	AALVAEYLSMLED-----HSYLPVGSVSFQNISSN		
HC2A	IDEEASMMEDVGMQD-----VHFNEVDVIMELLEQCADGLWKAERYELIADIYKLIPI		8.1
KIAA	IDEEASMMEDVGMQD-----VHFNEVDVIMELLEQCADGLWKAERYELIADIYKLIPI		
rat	IDEEASMMEDVGMQD-----VHFNEVDVIMELLEQCADGLWKAERLRAGLLTSINSSSP		
HC4	IDEEGAMKEDAGMMD-----VHYSEEVLLELLEQCVNGLWKAERYEIISEISKLGPI		
HC1	IKEEGAAKEDSGMHD-----TPYNEIILVEQLYMCGEFLWKSEYELIADVKNPIIAV		17.1/17.2
HC3	VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASFSGMAGMYEAVNEVYKVLPI		
HC5	VLEESVVSSEDTLSPDEGDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLPI		
ITAM ITAM ITAM ITAM			
HC2A	YEKRDR-----TYFRVAFVFGQAAQYQFTDSETDVE		9.1
KIAA	YEKRDRFERLAHIYDTLHRAYSKVTVMHSGRRLGTYFRVAFVFGQAAQYQFTDSETDVE		
rat	SMKSGGTLETHIYDTLHRAYSKVTVEVITR-----AGSWDLLPGGLFGQ		
HC4	YENRREFENLTQVYRTLHGAYTKILEVMHTKKRLG-----TYFRVAFVFGQ		
HC1	FEKQDFKFLSDIYYDIHRSYLKVAEVVNSEKRLFG-----TYFRVAFVFGQ		
HC3	HEANRDAKKLSTIHGKLQEAFFSKIYHQSTGWERMFG-----TYFRVGFYFG-		9.1
C5	LEAHREFRKLTLTHSKLQRAEDSIVNKDH--KRMFG-----TYFRVGFVFG-		
HC2A	-FFEDEDGKEYIYKEPKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA		10.1
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA		
rat	GFFEDEDGKEYIYKEPKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFA		
HC4	SFFEEEDGKEYIYKEPKLTGLSEISLRLVKLYGEKFGTENVKIIQSDSKVNAKELDPKYA		
HC1	GFFEEEGKEYIYKEPKLTGLSEISQRLCLKLYADKFGADNVKIIQSDSNKVNPKDLDPKYA		
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKA		10.1/10.2
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGCFCGAEFVEVIKDSNPVDKCKLDPNKA		4.1
HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRITILTA		11.1/11.2
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRITILTA		
rat	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRITILTA		
HC4	HIQVTYVKPYFDDKELTERKTEFERNHNISRFVFEAPYTLGKKQGCIEEQCKRRITILT		
HC1	YIQVTYVTPFFEEKEIEDRKTDFFEMHNNINRFVETPFTLGGKKHGGVAEQCKRRITILT		18.1
HC3	YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGEHQFRRKRTILT		
HC5	YIQITFVEPYFDEYEMKDRVITYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLT		

FIG. 6B (cont.)

		Coiled-Coil 1	Ref
HC2A	IHCFFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGQSV	
KIAA	IHCFFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLGQSV	
rat	IHCFFPYVKKRIPVMYQHHTDLNP	IEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLGQSV	
HC4	SNSFFPYVKKRIPINCEQQINLKP	IDGATDEIKDKTAELOKLCSSSTDVDMIQQLKLGQWV	
HC1	SHLFFPYVKKRIQVISQSSTELNP	IEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLGQSV	
HC3	SHAFPIKTRVNVTHKEEIIILTP	IEVAIEDMQKKTQELAFATHQDPADPKMLQMVLGQSV	11.1
HC5	MHAFFPIKTRISVIQKEEFVLTP	IEVAIEDMKKKTLLQAVAINQEPDAKMLQMVLGQSV	
		Coiled-Coil 2	
HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFROFVEACGQALAVNERLIKEDQLE		11.1/12.1
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFROFVEACGQALAVNERLIKEDQLE		
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFROFVEACGQALAVNERLIKEDQLE		
HC4	SVQVNAGPLAYARAFLLDSQASKYPPKKVSELKDMFRKFIQACSI ALELNERLIKEDQVE		
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFROFADACGQALDVNERLIKEDQLE		
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNKSLIGPVQKE		
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE		
		Coiled-Coil 2	
HC2A	YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPSTMTVHGMTSS		
KIAA	YQEEMKANYREMAKELSEIMHEQIC-----		
rat	YQEEMKANYREIRKELSDIIVPRICPGEDKRA TKFPAHLQRHQ RD TNKHSGSRV DQFILS		
HC4	YHEGLKSNFRDMVKELSDIIEHQILQEDTMHSPWMSNTLHVFC AISGTSSDRGYGSPRYA		
HC1	YQEELRSHYK DMLSELSTVMNEQITGRDDL SK---RGVDQTC TRVISKATPALPTVSISS		19.1
HC3	YQRELG---KLSS-----PZ-----		
HC5	YQQELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGSZ-		
	PEM		
HC2A	SSVVZ-----		
KIAA	-----		
rat	CVTLPEHPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMNGREKEPWTVI FNSRFYRSW GK		
HC4	EVL-----		
HC1	SAEVZ-----		
HC3	-----		
HC5	-----		
HC2A	-----		
KIAA	-----		
rat	VHIFF		
HC4	-----		
HC1	-----		
HC3	-----		
HC5	-----		

FIG. 6B (cont.)

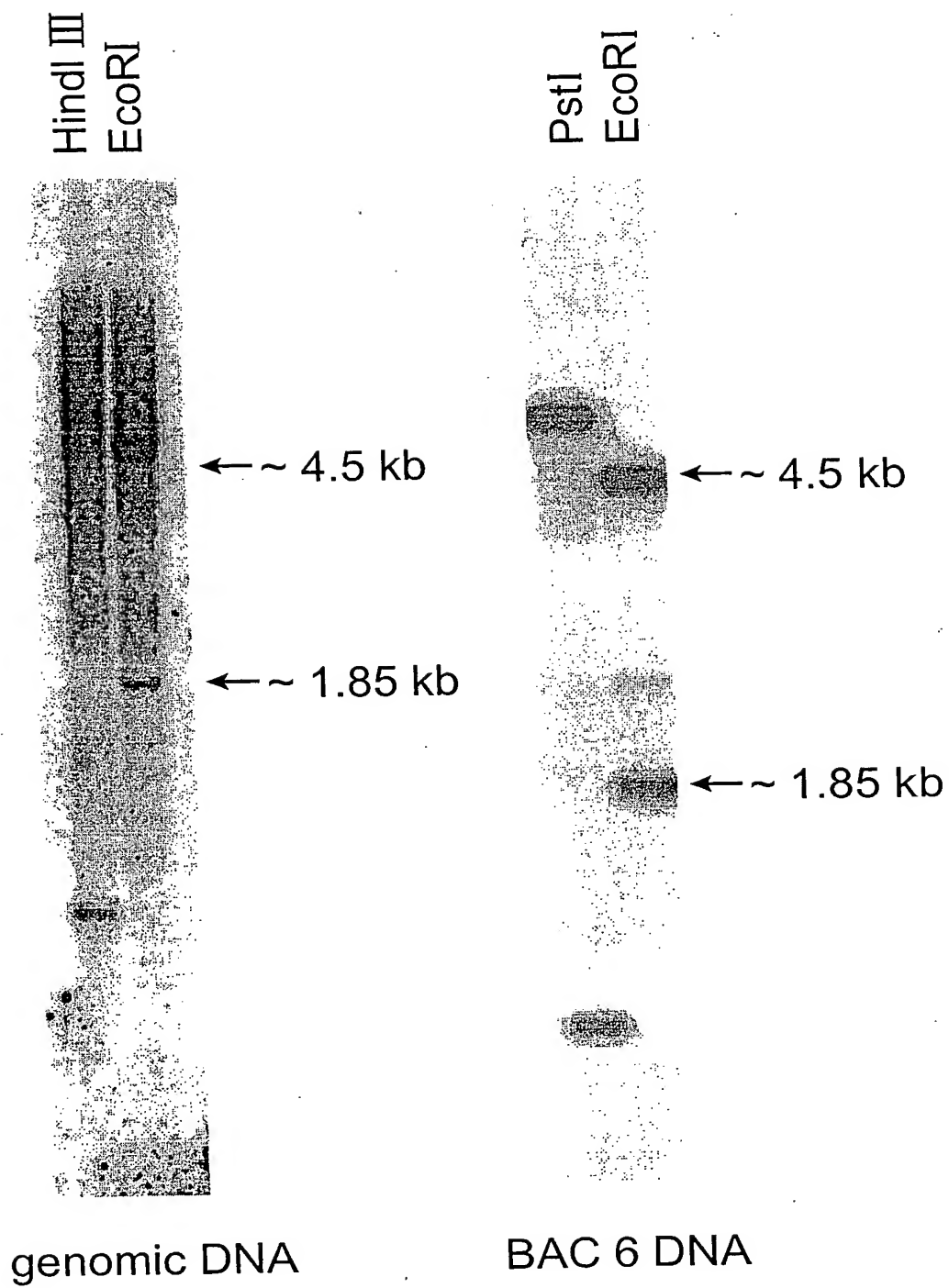


FIG. 7

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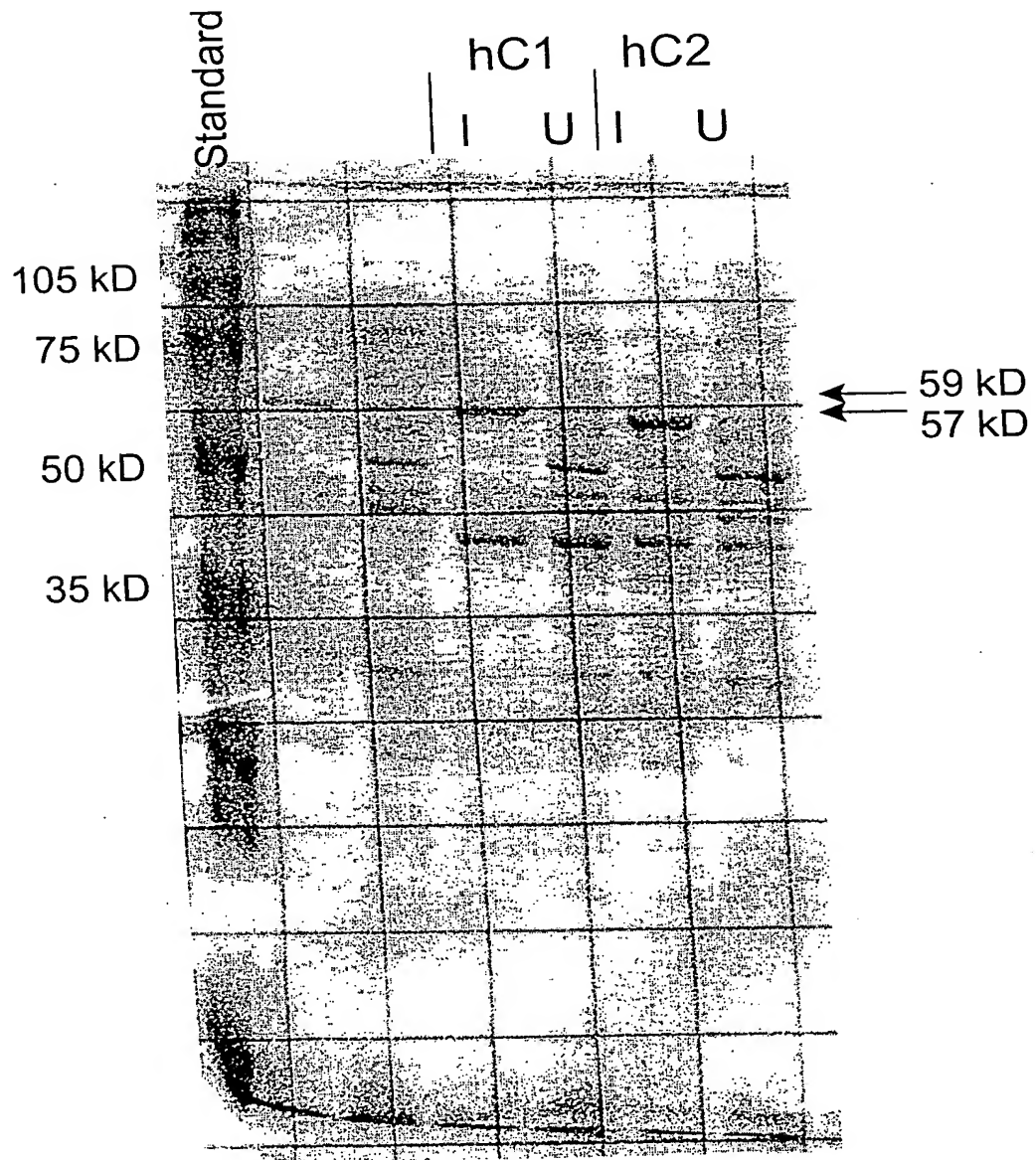


FIG. 8

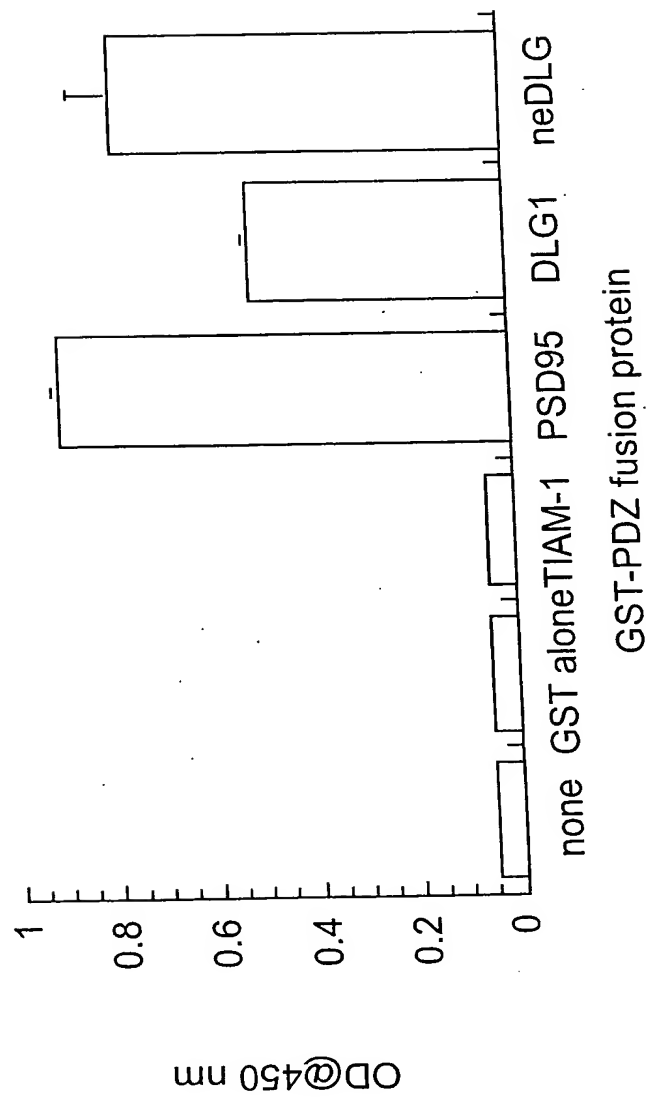


FIG. 9A

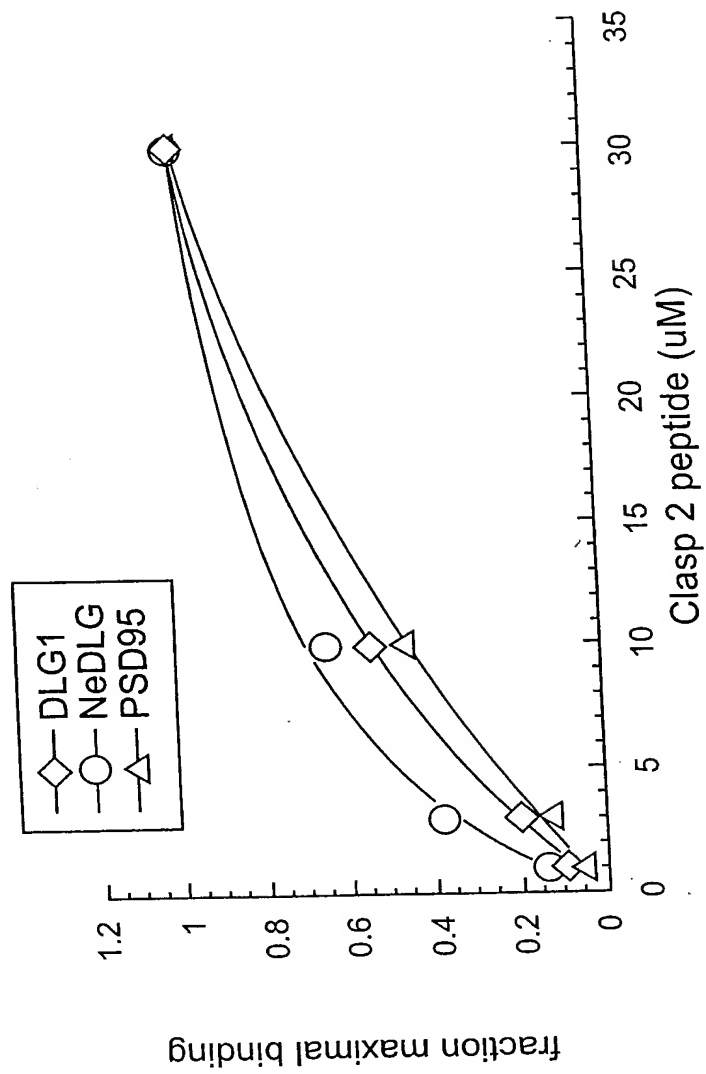


FIG. 9B

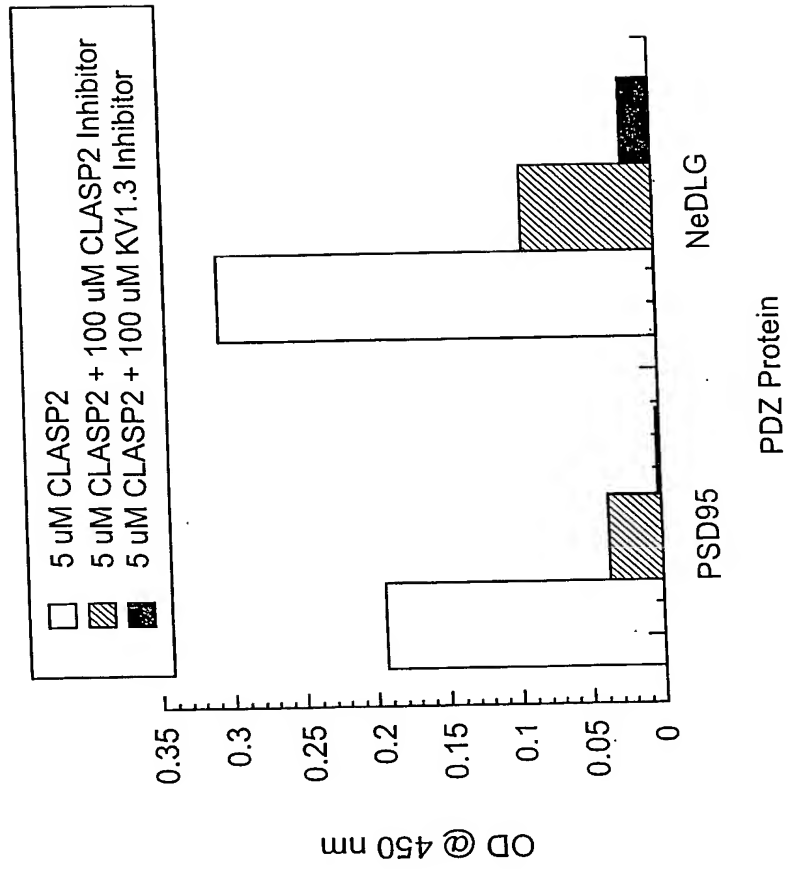


FIG. 9C

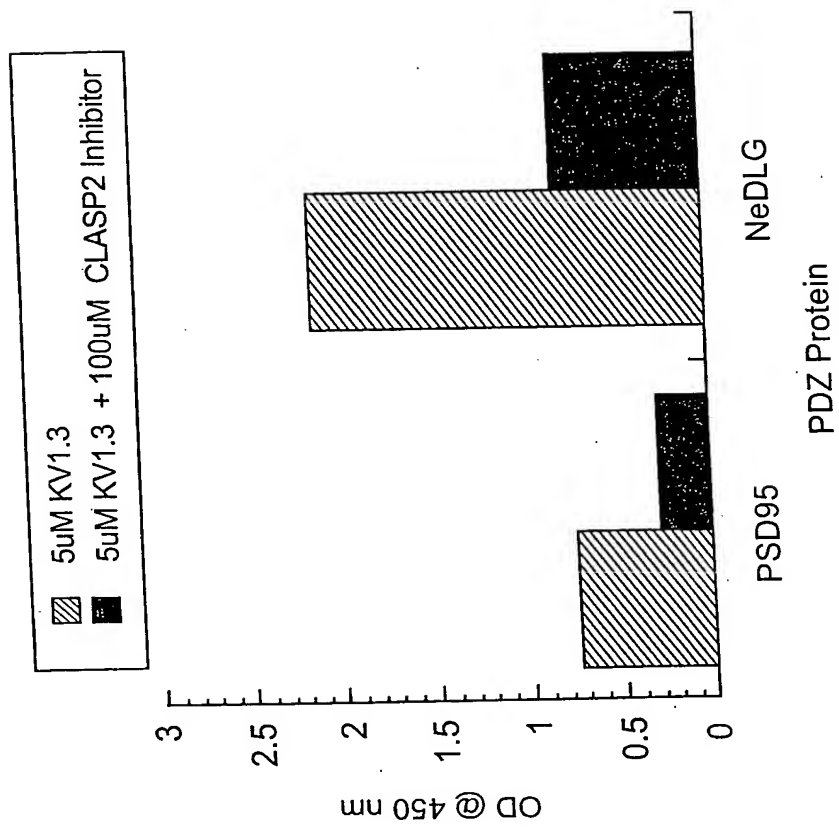


FIG. 9D

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC 80
81	GAATTCGGCA	CGAGTTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAT	AGAGTTGCC	ACTCAGCTGC 160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTGAG	CTGTGACAC	TCAAGTAAAG	GAAGCAGCAA	GAAGAGGGAT 240
241	GTCGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCCGAC	AGCACATCCC 320
321	GGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAATTAAT 400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA 480
481	ATTTTTTCCA	GTACTGTGAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACTTG	TAAAGTACCT	TAAGAGTCTG 560
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTC	CGAGTCTCCA	CCAGAGCCAC 640
641	ACAGGAAGAA	GTCCGGGTTA	ACGTGACTCG	GGTCATTAT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC 720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG 800
801	ACCAATCCA	TCACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCTCACCAG	CAACAACTA	CTGAGGTACT	CATGGTTTTT 880
881	CTTTGATGTA	CTGATCAAAT	CTATGGCTCA	GCATTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCCAAAC	CAGAGATTTT 960
961	CTGCATCCTA	TCATCATGCA	GCGGAAACCG	TTGTAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA 1040
1041	GAGGCATCTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCTTTGTCTT 1120
1121	CAAGCAGATC	AACAACCTACA	TTAGCTGTTT	TGCTCCTGGA	GAGCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC 1200
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACCT	GACCACTCCA	TTTGGAAGAG	GCAGGATTTA	AAGATACCAA 1280
1281	GACCTCCAGC	TTGACTACTC	ATTACAGAT	GAGTTCTGCA	AAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG 1360
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG 1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTCTC	CTGCCCTCTG	TTGGTCTGCT	TAAGTAAAC 1520
1521	GTCCAGCGGA	TCATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT 1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAAGC	ACCCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGCGGCCA 1680
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTCGAG	AGGATCTCTC 1760
1761	ATAAGCACAG	ATTCCGGTAA	CAGCCTTCCA	GAAGGAATA	GTGAGAAAG	CAATTCCCTG	GATAAGCACC	AACAAGTAGT 1840
1841	CACATTGGGA	AATTCCTGTG	TTCGCTGTGA	TAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA 1920
1921	TCTTAAAGAG	CATGCTGTAT	GATGCTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACCTATGGA	TTTTTTTACA 2000
2001	ATATCTGAAG	TCTGCCGTGA	CCAGTTCCAG	TACATGGGGA	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT 2080
2081	AGTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG 2160
2161	GCAGCCTGGA	TAACCTCTCT	ACTTTTAAAC	ACAGCTATGG	CCACTCGGAG	GCAGATGTTT	TGCACCGATC	ATTACTTGAA 2240
2241	GCCAACATTG	CTACTGAGGT	TTGCCGTGCA	GCTCTGGACA	CGCTTCTCT	ATTTACATTG	CGCTTTAAGA	ACCAGCTCCT 2320
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGTCTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA 2400
2401	CGGCTTTTAA	AAATGCTTTC	ACTGCCCTTAA	GGTCCCTAAT	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC 2480
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGGCTGT	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCAGCT 2560
2561	GCTCTAGTTC	CTGATGAGGA	ACAACCTTGA	TTACACTGGA	AAGAAGTCTT	TGTCCGGGAC	ACATTTGCAA	GTCAATCATAT 2640
2641	CTGTGAGCCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGGA	AACGAGATTG	CAGCAGTCCC	TGTCCATCAT	CAACAACCTG 2720
2721	GCCAACAGTG	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT	CTGATGTGAA	GGACTTAACC	AAAAGGATAC	GCACGGGTCT 2800
2801	AATGGCCACC	GCCAGATGTA	AGGAGCATGA	GAACGACCCA	GAGATCTGCG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT 2880
2881	ATGCCAGCAG	GCCGAGCTC	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG 2960
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AATATCTCAC	ACGGAAGGCG	GTGTTTAGAC	AAGGATGAC 3040
3041	CGCCTTCAGG	GCTATTACCC	CAAACATCGA	CGAGGAGGCC	TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTCCA 3120
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCGCAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC 3200
3201	ATCTACAAAC	TTATCATCCC	CATTTATGAG	AAGCGGAGGG	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTTACA 3280
3281	GGAAACCCAAA	CTCACACCGC	TGTCGGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTAATCGGA	TAAATTTGGT	TCTGAAATG 3360
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCACGTC 3440
3441	ATCCCTTCTT	TTGACGAAAA	AGAGTTGCAA	GAAGGAAAAA	CAGAGTTTGA	GAGATCCAC	AACATCCGCC	GCTTCATGTT 3520
3521	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGGCGGG	GTGGAAGAGC	AGTGCAAAAC	GCGCACCATC	CTGACAGCCA 3600
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCTAT	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC 3680
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGCGAGC	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT 3760
3761	CAAACTCCAG	GGCAGCGTGA	GTGTTCAAGT	CAATGCTGGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA 3840
3841	CAAAAGCGATA	TCTTGACAAT	AAAGTGAAGC	TGCTTAAAGTA	AGTTTTCAGG	CAATTGTGTT	AAGCTTGGCG	TTAAGCCCTTA 3920
3921	CGCGTAAACG	AACGTCTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG	AAATGGCGAA 4000
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT 4080
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTGCTGTT	ATTACATCTC 4160
4161	ATGGCCCGTG	TGTGGGACT	TGCTTTGTCA	TTTGCAAACT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA 4240
4241	CAGGAGGAGC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA 4320
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAAGTTTTT	ATTGTGCTTT	AACAAAGGTG	TGGTAGACAC 4400
4401	TCTTGAGCTG	GACTTAGATT	TTATTCTTCC	TTGCAGAGTA	GTGTAGAAAT	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG 4480
4481	ATCTACATGG	CAGGGAGGGC	TGCATGACA	TTGATGCTGT	GGGGACCTTT	TGCTCGAGT	CGTGCCGGAA	ATCTGATCTG 4560
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTTTGT	TAGGAGTATG	TTGATGACT	AGGATTGTGT	CTATTATCTC	ATTCAACAAC 4640
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTATTATA 4720
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA	CATTTTAAAT	ACTCACATGG	GCTTATGCTA	TAAGTTTAAAT 4800
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTTGTCAT	AAAAATGTGC	AATATGGAGA 4880
4881	TGTATACAAG	TCTTTACT						4898

FIG.10A

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	10	20	30	40	50	60	70	80						
1	MEGHVMI	PTILNQL	FRV L	TRATQEE	VA	VAQCHEE	SHLRSY	VKYA	YKAEPY	VASE	YKTVHEE	80		
81	SMTTILK	PSPA D	FLTSNKL	LR YSWFF	FDVLI	KSMAQH	LIEN		SKVKLL	RNR	FPASYH	HAAE	TVVNM	160
161	SKNANH	SLAV	FIKRCF	TFMD	RGFVFK	QINN	YISCF	APGDP	KTLFEY	KFEF	LRVVCN	HEHY	IPLNLP	240
241	QLDYSL	TDEF	CRNHFL	VGLL	LREVG	TALQE	FREVRL	IAIS	VLKNLL	IKHS	FDDRYA	SRSH	QARIAT	320
321	RINVRD	VSPF	PVNAGM	TVKD	ESLALP	AVNP	LVTPQK	KGSTL	DNSLHK	DLLG	AISGIA	SPYT	TSTPN	400
401	TDSGNS	LPER	NSEKSN	SLDK	HQQSST	LGNS	VVRCDK	KLDQS	EIKSLM	CFL	YILKSM	SDDA	LFTYWN	480
481	EVCLHQ	FQYM	GKRYIA	RNOE	GLGPIV	HDRK	SQTLFV	SRNR	TGMMHA	RLLQ	LGSLDN	SLTF	NHSYGH	560
561	IATEVCL	TAL	DTLSLF	TLLAF	KNQLLA	DHGH	NPLMKK	VFDV	YLCFLQ	KHQ	ETALKN	VETA	LRSLYK	640
641	AALCYE	ILKC	CNSKLS	SIRT	EASQLL	YFLM	RNNFDY	TGKK	SEVRTH	LQVI	ISVSQ	LIADV	VGIGET	720
721	SDRLIK	HTSF	SSDVKD	LTKR	IRTVLM	ATAQ	MKEHEN	DPEM	LVDLQY	SLAK	SYASTP	ELRK	TWLD	800
801	MCYVHV	TALV	AEYLTR	KGVE	RQGCTA	FRVI	TPNIDE	EASM	MEDVGM	QDVH	FNEDVL	MELL	EQCADG	880
881	KLIPIY	EKR	RDFE	DEDGK	EYIYKE	PKLT	PLSEIS	QRL	KLYSDK	FGSE	NVKMIQ	DSGK	VNPKDL	960
961	FFDEKE	LQER	KTEFER	SHNI	RRFM	FEMPFT	QTGKRQ	GGVE	EQCKRR	TILT	AIHCF	PYVK	RIPVMY	1040
1041	EMSKKV	AELE	QLCSSA	EVDM	IKLQLK	LQGS	VSVQVN	AGPL	AYARAF	LDDT	NTKRYP	DNKV	KLLKEV	1120
1121	NERLIK	EDQL	EYQEEM	KANY	REMAKE	LSEI	MHEQIC	PLEE	KTSVLP	NSLH	IFNAIS	GTPT	STMVHG	1195
	10	20	30	40	50	60	70	80						

FIG. 10A (cont.)

	10	20	30	40		50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	CCCCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC	80
81	GAATTCGGCA	CGAGTTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAT	AGAGTTGCC	ACTCAGCTGC	160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCAGGAA	GAAGAGGGAT	240
241	GTGCTTGAAA	CCCAAGTTGG	CTACTCTCTG	CTTCCCCTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC	320
321	GGTCTCGCGG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAATTTAAAT	400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA	480
481	ATTTTTCCTA	GTACTGTCTG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACTTG	TAAAGTACCT	TAAGAGTCTG	560
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCTTAAA	CCAGCTGTTC	CGAGTCCTCA	CCGAGGCCAC	640
641	ACAGGAAGAA	GTCGCGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC	720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGCGTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG	800
801	ACCAAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCTCTACCAG	CAACAACTA	CTGAGGTACT	CATGGTTTTT	880
881	CTTTGATGTA	CTGATCAAAT	CTATGGCTCA	GCATTTGATA	GAGAAGTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTC	960
961	CTGCACTCCTA	TCATCATGCA	GCGGAAACCG	TTGTAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA	1040
1041	GAGGCATCTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCTTTGTCTT	1120
1121	CAAGCAGATC	AACAACATA	TTAGCTGTTT	TGCTCTGGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC	1200
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACTT	ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AAGATACCAA	1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GAAACCACTT	CTTGGTGGGA	CTGTACTAGA	TGGAGTGGG	1360
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	GAGCTGTGTC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG	1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTTAC	CTGCCCTCTG	TTGGTCTGCT	GATTGAAAAC	1520
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT	1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCGCA	GAAGGGAAGC	ACCCCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGCGCCCA	1680
1681	TCTCCGCGAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTCGAG	AGGATCTCTC	1760
1761	ATAAGCACAG	ATTCCGGGTA	CAGCCTTCCA	GAAGGAATA	GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG	1840
1841	CACATTGGGA	AATTCCGTTG	TTGCTGTGTA	TAACTTTGAC	ACCTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA	1920
1921	TCTTAAAGAG	CATGCTCTGAT	GATGCTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACTTATGGA	TTTTTTTACA	2000
2001	ATATCTGAAG	TCTGCCTGCA	CCAGTTCCAG	TACATGGGGA	AGCGATATAC	AGCCAGGAAC	CAGGAGGGGT	TGGGACCAT	2080
2081	AGTTTATGAT	CGAAAGTCTC	AGACATGCCC	TGTTTCCCTG	CCACTCGGAC	GCAGATGTTT	TGCACCCAGT	ATTACTTGA	2160
2161	GCAGCCTGGA	TAACCTCTCT	ACTTTTAACC	ACAGCTATGG	CGCTTTTCTC	ATTACATTG	CGCTTTAAGA	ACCAGCTCCT	2240
2241	GCCAACTATT	CTACTGAGGT	TTGCCTGACA	GCTCTGGACA	GATGCTCTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA	2320
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAGTTTCTT	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC	2400
2401	CGGCTTTTAA	AAATGTCTTC	ACTGCCTTAA	GGTCTTTAAT	ACTTCAAGCT	GAGCTCCATC	AGGACGGAGT	CCTCCAGACT	2480
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGTCTGA	AAGAAGTCCCT	TTGTCCGGAC	ACATTGTCAA	GTCTATCAT	2560
2561	GCTCTACTTC	CTGATGAGGA	ACAACTTTGA	TTACATGGA	AACCAGATT	CAGCAGTCCC	TGTCCATCAT	CAACAAGTCT	2640
2641	CTGTTCAGCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGGA	CTGATGTGAA	GGACTTAACC	AAAAGGATAC	GCACGCTGCT	2720
2721	GCCAAACAGT	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT	2800
2801	AATGGCCACC	GCCCAGATGA	AGGAGCATGA	GAACGACCCA	CATGCCCAGG	ATCCATGTCA	AAAATGGGCA	TCTCTCAGAG	2880
2881	ATGCCAGCAC	GCCCAGGCTC	AGGAAGACGT	GGCTCGACAG	AAATATCTAC	ACGGAAGGCG	GTGTTAGAG	ACAGGCTGCT	2960
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	TCCATGATGG	AAGACGTGGG	GATGTCAGGAT	GTCCATTTC	3040
3041	CGCCTTCAGG	GTCTATTACC	CAAAACATCG	CGAGGAGGCC	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCCGCCAG	3120
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCGCAGA	ATTCTTTTGA	AGATGAAGAT	GGAAGGAGT	ATATTTCACA	3200
3201	ATCTACAAC	TTATCATCCC	CATTTATGAG	AAGCGGAGGG	TTCTCTTAA	TGTACTCGGA	TAAATTTGGT	TCTGAAAATG	3280
3281	GGAACCCAAA	CTCACACCGC	TGTCGGAAT	TTCTCAGAGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCAGCTT	3360
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	CAGAGTTTGA	GAGATCCCAC	AACATCCGCC	GCTTCATGTT	3440
3441	ATCCCTTCTT	TTGACGAAAA	AGAGTTGCAA	GAAGGAAAA	GTGGAAGAGC	AGTGCAAACG	CGCCACCATC	CTGACAGCCA	3520
3521	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGGCCGG	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC	3600
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCTAT	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT	3680
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGCGCAG	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA	3760
3761	CAAACCTCCAG	GGCAGCGTGA	GTGTTCAAGT	CAATGCTGGC	AGTTTTTCAGG	CAATTTGTGG	AAGCTTGCGG	TCAAGCCTTA	3840
3841	CAAAGCAGATA	TCCTGACAA	AAAGTGAAGC	TGCTTAAGGA	ATCAGGAAGA	AATGAAAGCC	AACATACAGG	AAATGGCGGA	3920
3921	GCGGTAAACG	AACGCTCTGAT	TAAAGAAAGC	CAGCTCGAGT	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT	4000
4001	GGAGCTTTCT	GAATCATGCT	ATGAGCAGAT	CTGCCCCCTG	CGGGATGACC	AGCTCGTCTT	CGGTCTGTGT	ATTACATCTC	4080
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA	4160
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACT	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA	4240
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	CRAAGTTTTC	ATTGTGTCTT	AACAAAGGTG	TGGTAGACAC	4320
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	GTGTTAGAAT	AGATGGCCTA	CGTGCCGGAA	ATCTGATCGT	4400
4401	TCTTGAGCTG	GACTTAGATT	TTATCTCTCC	TTGCAGAGTA	GGGACCTTTT	TGCCCTGACT	CGTGCCGGAA	ATCTGATCGT	4480
4481	ATCTACATGG	CAGGGAGGGC	TGCACCTGAC	TTGATGCTGG	TTGTATGACT	AGGATTGTGT	CTATTATCTC	ATTCAACAAC	4560
4561	AATCAGGGTA	CAGAACCTAC	TAGTTTTGTC	TAGGAGTATG	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TGTGATTTAA	4640
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	CATTTTAAAT	ACTCACATGG	GCTTATGCAT	TAAGTTTAA	4720
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA	TAATGGTTTA	TTCTGTCTAT	AAAAATGTGC	AATATGGAGA	4800
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT					4880
4881	TGTATACAAG	TCTTTACT							4898

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	10	20	30	40	50	60	70	80	
1	MEGHVMAFL	PTILNQLFRV	LTRATQEEVA	VNVTRVHHV	VAQCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK	80
81	SMTTILKPSA	DFLTSNKLLR	YSWFFFDVLI	KSMAQH LIEN	SKVKLLRNQR	FPASYHHAAE	TVVNMLMPHI	TQKFGDNPEA	160
161	SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNHEHY	IPLNLPMPFG	KGRIQRYQDL	240
241	QLDYSLTDEF	CRNHFLVGLL	LREVGTA LQE	FREVRLIAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ	320
321	RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPOKGSTL	DNSLHKDLLG	AISGLASPYT	TSTPNINSVR	NADSRGSLIS	400
401	TDSGNSLPER	NSEKSNSLDK	HQSSSTLGNS	VVRCDKLDQS	EIKSLLMCFL	YILKSMSDDA	LETTYWNKAST	SEIMDFFTIS	480
481	EVCLHQFQYM	GKRYIARNQE	GLGPIVHDRK	SQTLPVSRNR	TGMMHARLQQ	LGSLDNSLTF	NHSYGHSDAD	VLHQSLLEAN	560
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVEDV	YLCFLQKHQS	ETALKNVFTA	LRS LIYKFPS	TFYEGRADMC	640
641	AALCYEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGKK	SEVVRTHLQVI	ISVSQLIADV	VGIGETRFQQ	SLSIINN CAN	720
721	SDRLIKHTSF	SSDVKDLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLD SMARIH	VKNGDLSEAA	800
801	MCYVHVHTALV	AEYLTRKGVF	RQCCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY	880
881	KLIPIIYEKR	RDFEDEDGK	EYIYKEPKLT	PLSEISQRLI	KLYSDKFGSE	NVKMIQDSGK	VNPKDLD SKY	AYIQVTHVIP	960
961	FFDEKELQER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFFPVVKK	RIPVMYQHHT	DLNPIEVAID	1040
1041	EMSKKVAELR	QLCSSAEVDM	IKLQLKLQGS	VSVQVNAGPL	AYARAFLLDT	NTKRYPDNKV	KLLKEVFRQF	VEACGOALAV	1120
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPT	STMVHGMTSS	SSVV	1195
	10	20	30	40	50	60	70	80	

FIG. 10B (cont.)

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	CCCCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC 80
81	GAATTCGGCA	CGAGTTTTC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAT	AGAGTTGCCC	ACTCAGCTGC 160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTACG	CTGTGACAAC	TCAAGTAAAG	GAAGCACGAA	GAAGAGGGAT 240
241	GTGCTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCTCCTC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC 320
321	GGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAATTTAAAT 400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA 480
481	ATTTTGTCCA	GTACTGTGAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGAGTCTG 560
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTC	CGAGTCTCTA	CCAGAGCCAC 640
641	ACAGGAAGAA	GTCGCGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC 720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG 800
801	ACCAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCCCTCACCAG	CAACAAACTA	CTGAGGTACT	CATGGTTTTT 880
881	CTTTGATGTA	CTGATCAAAAT	CTATGGCTCA	GCATTTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCCAAAC	CAGAGATTTT 960
961	CTGCTACCTA	TCATCATGCA	GCGGAAACCG	TTGTAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA 1040
1041	GAGGCACTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCTTTGTCTT 1120
1121	CAAGCAGATG	AACAACATACA	TTAGCTGTTT	TGCTCCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC 1200
1201	GTGTTAGTGT	CAACCATGAA	CATTATATTC	CGTTGAACCT	ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AAGATACCAA 1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG 1360
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG 1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCCCTTAC	CTGCCCTGT	TTGGTCTGCT	GATTGAAAAA 1520
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT 1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCGCGA	GAAGGGAARG	ACCTGTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA 1680
1681	TCTCCGCGAT	TGCTTCTCCA	TATACAACCT	CACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTCGAG	AGGATCTCTC 1760
1761	ATAAGCACAG	ATTCGGGTAA	CAGCCTTCCA	GAAGGAATA	GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAGTAG 1840
1841	CATTCTGGGA	AATTCCTGTG	TTGCTGTGTA	TAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA 1920
1921	TCTTAAAGAG	CATGCTGTAT	GATGCTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACCTTATGA	TTTTTTTACA 2000
2001	ATATCTGAAG	TCTGCCTGCA	CCAGTTCAG	TACATGGGGA	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT 2080
2081	AGTTCAATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG 2160
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAACC	ACAGCTATGG	CCACTCGGAC	GCAGATGTC	TGCACCAATC	ATTACTTGAA 2240
2241	GCCAAACATTG	CTACTGAGGT	TTGCCTGACA	GCTCTGGACA	CGCTTCTCT	ATTTACATTG	GCGTTTAAAG	ACCAGCTCCT 2320
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGTCTACC	TGTGTTTTCT	TCAAAAACAT	CAGCTTGAAA 2400
2401	CGGCTTTAAA	AAATGTCTTC	ACTGCCTTAA	GGTCCCTTAAT	TATATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC 2480
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGTGTGA	ACTCCAAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCAGCT 2560
2561	CTCTACTTTC	CTGATGAGGA	ACAACTTTGA	TTAACTTGGA	AAGAAGTCCCT	TTGTCCGGAC	ACATTTGCAA	GTCTCATAT 2640
2641	GCTGTACGCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGGA	AACCAGATTG	CAGCAGTCCC	TGTCCATCAT	CAACAACGT 2720
2721	GCCAAACAGTG	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT	CTGATGTGAA	GGACTTAAAC	AAAAGGATAC	GCACGGTGCT 2800
2801	AATGGCCACC	GCCCAGATGA	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCC 2880
2881	ATGCCAGCAC	GCCCAGGCTC	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG 2960
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AAATATCTCAC	ACGGAAGGCC	GTGTTTAGAG	AAGGATGCAC 3040
3041	CGCCTTCAGT	GTCAATTACC	CAAAACATCGA	CGAGGAGGCC	TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTTC 3120
3121	ACGAGGATGG	GCTGATGGAG	CTCCTTGAGC	AGTGCCGAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC 3200
3201	ATCTACAAAC	TTATCATCCC	CATTTATGAG	AAGCGGAGGG	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTACAA 3280
3281	GGAAACCCAAA	CTCACACCGC	TGTCGGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAATG 3360
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCAGCTC 3440
3441	ATCCCTTCTT	TTGACGAAAA	AGAGTTGCAA	GAAGGAAAAA	CAGAGTTTGA	GAGATCCAC	AACATCCGCC	GCTTCATGTT 3520
3521	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGGCGGG	GTGGAAGAGC	AGTGCAAACG	GCGCACCATC	CTGACAGCCA 3600
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCTAT	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC 3680
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT 3760
3761	CAAATCCAG	GGCAGCGTGA	GTGTTCAAGT	CAATGCTGGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA 3840
3841	CAAAGCGATA	TCCTGACAAAT	AAAGTGAAGC	TGCTTAAAGGA	AGTTTTTCAGG	CAATTTGTGG	AAGCTTGGCG	TCAAGCCTTA 3920
3921	GCGGTAAACG	AACGTCTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACACAGGG	AAATGGCGAA 4000
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCTCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTC	CTTCACATCT 4080
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTCTGTGT	ATTACATCTC 4160
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA 4240
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACAAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGAGTTTGT 4320
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAAGTTTTC	ATTGTGCTCT	AACAAAGGTG	TGGTAGACAC 4400
4401	TCTTGAGCTG	GACTTAGATT	TTATTCTTCC	TTGCAGAGTA	GTGTTAGAAAT	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG 4480
4481	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCGCTG	GGGGACCTTT	TGCCCTCGACT	CGTGCCGGAA	ATCTGATCGT 4560
4561	AATCAGGGTA	CAGAACCTTAC	TAGTTTGTCT	TAGGAGTATG	TTGTATGACT	AGGATTTGTG	CTATTATCTC	ATTCAACAAC 4640
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCAATTA 4720
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA	CATTTTAAAT	ACTCAGATGC	GCTTATGCAT	TAAAGTTTAA 4800
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTTGTCAT	AAAAATGTGC	AATATGGAGA 4880
4881	TGTATACAAG	TCTTTACT						

FIG.10C

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	10	20	30	40	50	60	70	80	
1	MEGHVMI	PTILNQLFRV	LTRATQEEVA	VNVTRVHHV	VAQCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK	80
81	SMTTILKPSA	DFLTSNKLLR	YSWFFFDVLI	KSMAQHLIEN	SKVKLLRNQR	FPASYHHAEE	TVVNMLMPHI	TQKFGDNPEA	160
161	SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLEFYKFEF	LRVVCNHEHY	IPLNLPMPFG	KGRIQRYQDL	240
241	QLDYSLTDEF	CRNHFLVGLL	LREVGTAQOE	FREVRLIAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ	320
321	RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPOKGSTL	DNSLHKDLLG	AISGIASPYT	TSTPNINSVR	NADSRGSLIS	400
401	TDSGNSLPER	NSEKSNSLDK	HQSSSTLGNS	VVRCDKLDQS	EIKSLIMCFL	YILKSMSDDA	LFTYWNKAST	SELMDEFTIS	480
481	EVCLHQFYQM	GKRYIARNQE	GLGPVHDKR	SQTLPVSRNR	TGMMHARLQQ	LGSLDNLSTF	NHSYGHSDAD	VLHQSLLEAN	560
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC	640
641	AALCYEILKC	CNSKLSSTRT	EASQLLYFLM	RNNFDYTGKK	SFVRTHLQVI	ISVSQLIADV	VGIGETRFQQ	SLSIINNCAN	720
721	SDRLIKHTSF	SSDVKOLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLDSEARH	VKNIGDLSEA	800
801	MCYVHVITALV	AEYLTRKGVF	RQCCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY	880
881	KLIPIYIEKR	RDFEDEDGK	EYIYKEPKLT	PLSEISQRLL	KLYSDKFGSE	NVKMIQDSGK	VNPKDLDSKY	AYIQVTHVIP	960
961	FFDEKELQER	KTEFERSHNI	RREFMEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFPPYVKK	RIPVMYQHHT	DLNPIEVAID	1040
1041	EMSKKVAELR	QLCSSAEVDM	IKLQLKLQGS	VSVQVNAGPL	AYARAFLLDT	NTKRYPDNKV	KLLKEVFRQF	VEACGQALAV	1120
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPT	STMVHGMTSS	SSVV	1195
	10	20	30	40	50	60	70	80	

FIG. 10C (cont.)

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCC	GAGGTGACG	GTATCGATAA	GCTTGATATC
81	GAATTCGGCA	CGAGTTTATC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAT	AGAGTTGCC	ACTCAGCTGC
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCTAG	CTGTGACAA	TCAAGTAAAG	GAAGCAGGAA	GAAGAGGGAT
241	GTCTGTTGAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCCGAGC	AGCACATCCC
321	GGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAATTTAAAT
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA
481	ATTTTTTCCA	GTACTGTCTG	AAAACCGAAT	CTGGAGCCCC	AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGAGTCTG
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTC	CGAGTCTCTA	CCAGAGGCCAC
641	ACAGGAAGAA	GTCCGCGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAAGCTG
801	ACCAAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCTCACCCAG	CAACAACTA	CTGAGGTACT	CATGGTTTTT
881	CTTTGATGTA	CTGATCAAA	CTATGGCTCA	GCATTTGATA	GAGAATCCCA	AAGTTAAGTT	GCTGCCGAAC	CAGAGATTTT
961	CTGCATCCTA	TCATCATGCA	GCGGAAACCG	TTGTAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA
1041	GAGGCACTTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAGAGATG	TTTCCACTTC	ATGGACAGGG	GCTTTGTCTT
1121	CAAGCAGATC	AACAACCTA	TAGCTGTTT	TGCTCCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACTT	ACCAATGCCA	TTTGGAAAG	GCAGGATTC	AAGATACCAA
1281	GACCTCCAGC	TTGACTACTC	ATTACAGAT	GAGTTCTGCA	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTAC	CTGCCCTGT	TTGGTCTGCT	GATTGAAAAC
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	CACCTCTAC	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCGCA	GAAGGGAAGC	ACCCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTCGAG	AGGATCTCTC
1761	ATAAGCACAG	ATTCGGGTAA	CAGCCTTCCA	GAAAGGAATA	GTGAGAAAG	CAATTCCTTG	GATAAGCACC	AACAAAGTAG
1841	CACATTGGGA	AATCCGCTGG	TTGCTGTGTA	TAAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA
1921	TCTTAAAGAG	CATGCTGTAT	GATGCTTTGT	TTACATATTT	GAACAAGGCT	TCAACATCTG	AACCTTATGA	TTTTTTTACA
2001	ATATCTGAAG	TCTGCCCTGCA	CCAGTTCAG	TACATGGGGA	AGCCATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT
2081	AGTTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAAAC	ACAGCTATGG	CCACTCGGAC	GCAGATGTTT	TGCACCATG	CCCTGGCTCT
2241	GCCAAACATT	CTACTGAGGT	TTGCTGTGCA	GCTCTGGACA	CGTCTCTCTC	ATTTTACATT	GCGTTTAAAG	ACCAGCTCCT
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGTCTTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA
2401	CGGCTTTAAA	AAATGTCTTC	ACTGCCCTTAA	GGTCCCTTAA	TTATAAGTTT	CCCTCAACAT	TCATGAAGG	GAGAGCGGAC
2481	ATGTTGTGCG	CTCTGTGTTA	CGAGATTCTC	AAGTGCTGTA	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCAGGCT
2561	GCTCTACTTC	CTGATGAGGA	ACAACCTTGA	TTACACTGGA	AAGAAGTCTC	TGTCCGGAC	ACATTTGCAA	GTCATCATAT
2641	CTGTACGCCA	GCTGATAGCA	GACGTGTGTT	GCATTGGGGA	AACCAGATT	GGACTTAACC	AAAAGGATAC	GCACGGTGCT
2721	GCCAAACAGT	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT	CTGATGTGAA	GGACTTAACC	AAAAGGATAC	GCACGGTGCT
2801	AATGGGCCAC	GCCAGATGAT	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT
2881	ATGCCAGCAC	GCCGAGCTC	AGGAAGACGT	GGCTGCGACG	CATGGCCAGG	ATCCATGTCA	AAAATGGCCA	CTCTCTCAGG
2961	CGAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AAATATCTAC	ACGGAAGGCG	GTGTTTAGAC	AAGGATGCAC
3041	CGCCTTACAG	GTCATTACCC	CAAAACATCGA	CGAGGAGGCC	TCCATGATGG	AAGACGTGGG	GATGACAGGT	GTCCATTCCA
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGGCGAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC
3201	ATCTACAAAC	TTATCATCCC	CATTTATGAG	AAGCGGAGGG	ATTTCTTTGA	AGATGAAGAT	GGAAGGAGT	ATATTTACAA
3281	GGAAACCCAAA	CTCACACCCG	TGTCGGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAAATG
3361	TCAAATATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCAGCTC
3441	ATCCCTTTCT	TTGACGAAAA	AGAGTTGCAA	GAAAGGAAAA	CAGAGTTTGA	GAGATCCAC	AACATCCGCC	GCTTCATGTT
3521	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGGCGGG	GTGGAAGAGC	AGTGCAACG	GCGCACCATC	CTGACAGCCA
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCTTGTCAT	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC
3681	ATTGACGAGA	TGAGTAAGAA	GCTGGCGGAG	CTCCGCGCAG	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT
3761	CAAACTCCAG	GGCAGCGTGA	GTGTTCAAGT	CAATGCTGGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA
3841	CAAAGCGATA	TCCTGACAAT	AAAGTGAAGC	TGCTTAAAGGA	AGTTTTTCA	CAATTTGTGG	AAGCTTGGCG	TCAAGCCTTA
3921	GGGTTAAACG	AACGTCTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG	AAATGGCGAA
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCTCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTC	CTTCACATCT
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTGCTGTG	ATTACATCTC
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTTGAAACT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAATAAAG	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAAGTTTTT	ATTGTGTCTT	AACAAGGTTG	TTTATTACAC
4401	TCTTGAGCTG	GACTTAGATT	TTATCTTCTC	TTGCAGAGTA	GTGTTAGAA	AGATGGCCTA	CAGAAAAA	AGGTTCTGGG
4481	AATCTACATG	CAGGAGGGG	TGCACTGACA	TTGATGCTG	GGGGACCTTT	TGCTCGACT	CGTGCCGGAA	ATCTGATCGT
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTTGTC	TAGGAGTATG	TTGATGACT	AGGATTTGTG	CTATTATCTC	ATTCAACAA
4641	ATAGAGCAAG	AATAGTGAG	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCATTAA
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA	CATTTTTTAA	ACTCACATGG	GCTTATGCAT	TAAGTTTAA
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTGTGTC	AAAAATGTGC	AATATGGAGA
4881	TGTATACAAG	TCTTTACT						4898

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		10		20		30		40		50		60		70		80		
1	MEGHV	MIAFL	PTILN	QLFRV	LTRAT	QEEVA	VNVTR	VIIHV	VAQC	CHEGLE	SHLRS	YVKYA	YKAEP	YVASE	YKTV	HEELTK	80	
81	SMTTIL	KPSA	DELT	SNKLLR	YSWFF	FDVLI	KSMAQ	HLIEN	SKVK	LLRNQR	FPASY	HHAEE	TVVNM	LMPHI	TQKFG	DNPEA	160	
161	SKNANH	SLAV	FIKRC	FTFMD	RGFVF	KQINN	YISCF	APGDP	KTLE	FEYKFEF	LRVVC	NHEHY	IPLN	LPMFPG	KGRIQ	RYQDL	240	
241	QLDYSL	TDEF	CRNH	FLVGLL	LREVG	TALQE	FREVRL	IAIS	VLKN	LLIKHS	FDDRY	ASRSH	QARI	ATLYLP	LFGLL	IENTVQ	320	
321	RINVRD	VSPF	FVNAG	MTVKD	ESLAL	PAVNP	LVTPO	KGSTL	DNSL	HKDLLG	AISGL	ASPYT	TSTPN	INSVR	NADSR	GSLIS	400	
401	TDSGNS	LPER	NSEKS	NSLDK	HQOSS	TLGNS	VVRCD	KLDQS	EIKSL	LMCFL	YILKS	MSDDA	LEFTY	WNKAST	SELM	DFFTIS	480	
481	EVCLHQ	FQYM	GKRYI	ARNQE	GLGPI	VHDRK	SQTLF	VSRNR	TGMM	HARLQ	Q	LGSLD	NSLTF	NHSYG	HSAD	VLHQ	SLEAN	560
561	IATEV	CLTAL	DTLS	LFTLAF	KNQLL	ADHGH	NPLMK	KVFDV	YLCF	LQKHQS	ETALK	KNVFTA	LRSLI	YKFPS	TFYEG	RADMC	640	
641	AALCYE	ILKC	CNSKL	SSIRT	EASQL	LYFLM	RNNED	YTGKK	SEFVR	THLQVI	ISVSQ	LIADV	VGIGET	RFQ	Q	SLSI	INNCAN	720
721	SDRLIK	HTSF	SSDVK	DLTKR	IRTVL	MATAQ	MKEHE	NDEP	LVDL	QYSLAK	SYAST	PELRK	TWLD	SMARIH	VKNGD	LSEAA	800	
801	MCYVHV	TALV	AEYL	TRKGVF	RQGCT	AERVI	TPNID	EEASM	MEDVG	MQDVH	FNEDV	LMELL	EQCAD	GWLKA	ERYEL	IADIY	880	
881	KLIPIY	EYKR	RDFFE	DEDGK	EYIYK	EPKLT	PLSEI	SQRLL	KLYSD	KFGSE	NVKMI	QDSGK	VNPKD	LDSKY	AYIQV	THVIP	960	
961	FFDEKE	LQER	KTEFE	RSJNI	RREMF	FEMPFT	QTGKR	QGGVE	EQCKR	RTILT	AHCFF	PYVKK	RIPVM	YQHHT	DLNPI	EVAVD	1040	
1041	EMSKKV	AEALR	QLCSS	AEVDM	IKLQL	KLQGS	VSVQV	NAGPL	AYARA	FLDDT	NTKRY	PDNKV	KLLKE	VFRQF	VEACG	QALAV	1120	
1121	NERLIK	EDQL	EYQEE	MKANY	REMAK	ELSEI	MHEQI	CPLLE	KTSVL	ENSLH	IFNAI	SGTPT	STMVH	GMTSS	SSVV		1195	
		10		20		30		40		50		60		70		80		

FIG. 10D(cont.)

	10	20	30	40	50	60	70	80	
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	CCCCCCCCCTC	GAGGTGACAG	GTATCGATAA	GCTTGATATC	80
81	GAATTCGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAAAT	AGAGTTGCCC	ACTCAGCTGC	160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCTG	CTGTGACAAC	TCAAGTAAAG	GAAGCACGAA	GAAGAGGGAT	240
241	GTCGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCCCTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC	320
321	GGTCTCGCG	AACCTTCCCT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAAT	400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA	480
481	ATTTTTTCCA	GTACTGTGAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGAGTCTG	560
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTC	CGAGTCTCTA	CCAGAGCCAC	640
641	ACAGGAAGAA	GTGCGGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC	720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG	800
801	ACCAATATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCCTCACCAG	CAACAACTA	CTGAGGTACT	CATGGTTTTT	880
881	CTTTGATGTA	CTGATCAAAT	CTATGGCTCA	GCATTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTT	960
961	CTGCATCCTA	TCATCATGCA	GCGGAAACCG	TTGTAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA	1040
1041	GAGGCATCTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCCTTGTCTT	1120
1121	CAAGCAGATC	AACAACCTACA	TTAGCTGTTT	TGCTCCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC	1200
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACCT	ACCAATGCCA	TTTGGAAGAAG	CGAGGATCCA	AGATACCAA	1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG	1360
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG	1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCCCTTAC	CTGCCCTCTG	TTGGTCTGCT	GATTGAAAC	1520
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT	1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAAGC	ACCTTGAGCA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA	1680
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTCGAG	AGGATCTCTC	1760
1761	ATAAGCACAG	ATTCGGGTAA	CAGCCTTCCA	GAAAGGAATA	GAACCACTT	GTGAGAAATG	GATAAGCACC	AACAAAGTAG	1840
1841	CACATTGGGA	AATTCCGTGG	TTGCTGTGTA	TAAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA	1920
1921	TCTTAAAGAG	CATGCTCTGAT	GATGCTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACCTTATGA	TTTTTTTACA	2000
2001	ATATCTGAAG	TCTGCCTGCA	CCAGTTCCAG	TACATGGGGA	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT	2080
2081	AGTTTCATGAT	CTGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	AACAGAACAG	GAATGATGCA	TGCCAGATTC	CAGCAGCTGG	2160
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAAAC	ACAGCTATGG	CCACTCGGAC	GCAGATGTTC	TGCACGATC	ATTACTTGAA	2240
2241	GCCAAACATTG	CTACTGAGGT	TTGCCCTGACA	GCTCTGGGGA	CGCTTTCTCT	ATTTACATTG	CGGTTTAAAG	ACCAGCTCCT	2320
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGTCTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA	2400
2401	CGGCTTTTAA	AAATGTCTTC	ACTGCCCTAA	GGTCCTTAAT	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAG	2480
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTCTGTGA	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCAGCT	2560
2561	GCTCTACTTC	CTGATGAGGA	ACAACTTTGA	TTACACTGGA	AAGAAGTCCT	TTGTCCGGAC	TGTCCATCAT	CAACAACCTG	2640
2641	CTGTGAGCCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGGA	AACAGATTTC	CAGCAGTCCC	TGTCCATCAT	CAACAACCTG	2720
2721	GCCAAACAGTG	ACCGGCTTAT	TAAAGCACCC	AGCTTCTCCT	CTGATGTGAA	GGACTTAAAC	AAAAGGATAC	GCACGGTCTC	2800
2801	AGTTGCGGAG	GCCAGATGTA	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT	2880
2881	ATGCCAGCAC	GCCCGAGCTC	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG	2960
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AAATATCTCAC	ACGGAAGGCG	GTGTTTAGAC	AAGGATGCAC	3040
3041	CGCCTTCAGG	GCTCATTACC	CAAAACATCGA	CGAGGAGGCC	TCCATGATGG	AAGACGTGGG	GATGACAGAT	GTCCATTCTA	3120
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCCGAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC	3200
3201	ATCTACAAAC	TTATCATCCC	CATTTATGAG	AAGCGGAGGG	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTACAA	3280
3281	GGAAACCCAAA	CTCACACCGC	TGTCGGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAAATG	3360
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCTTAAGGA	TCTGGATTCT	AAGTATGCCA	AACATCCGCC	GCTTCATGTT	3440
3441	ATCCCCCTCT	TTGACGAAAA	ACAGTTGCAA	GAAAGGAAAA	CAGAGTTTGA	GAGATCCAC	AACATCCGCC	GCTTCATGTT	3520
3521	TGAGATGCCA	TTTACGCGAG	CCGGGAAGAG	GCAGGGCGGG	GTGGAAGAGC	AGTGCAAAAC	GCGCACCATC	CTGACAGCCA	3600
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCTG	GTACCAGCAC	CACACTGACC	GACATGATCA	AAGTGCAGCT	3680
3681	ATTGACGAGA	TGAGTAAGAA	GGTGCGGAG	CTCCGGCAGC	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AAGTGCAGCT	3760
3761	CAAACTCCAG	GGCAGCGTGA	GTGTTTCAGG	CAATGCTGGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA	3840
3841	CAAAGCGATA	TCTTGACAAAT	AAAGTGAAGC	TGCTTAAAGG	AGTTTTCAGG	CAATTTGTGG	AAGCTTGCGG	TCAAGCCTTA	3920
3921	GCGGTAAACG	AACGCTGTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACATACAGG	AAATGGCGAA	4000
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTC	CTTCACATCT	4080
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTGCTGTG	ATTACATCTC	4160
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGGAACCT	CAGGATTTGA	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA	4240
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAATAAAG	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA	4320
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAT	TGGCAATATT	CAAAGTTTTC	ATTGTGTCTT	AACAAGAGTG	TGGTAGACAC	4400
4401	TCTTGAGCTG	GACTTAGATT	TTATTTCTCC	TGTCAGAGTA	GTGTTAGAAAT	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG	4480
4481	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCCTG	GGGGACCTTT	TGCCCTCGACT	CGTGCCGGAA	ATCTGATCGT	4560
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTGTGC	TAGGAGTATG	TTGTATGACT	AGGATTTGTG	CTATTATCTC	ATTAACAAC	4640
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGCGTTCA	AGTCAGAACT	TTGTCAATTA	4720
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA	CATTTTAAAT	ACTCACATGG	GCTTATGCAT	TAAGTTTAAAT	4800
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATCACTT	TAATGTTTAA	TTCTTGTCAT	AAAAATGTGC	AATATGGAGA	4880
4881	TGTATACAAG	TCCTTACT							4898

FIG.10E

	10	20	30	40	50	60	70	80
1	MEGHVMI	PTILNQLFRV	LTRATQEEVA	VNVTRVHHV	VAQCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK 80
81	SMTTILKPSA	DELTSTNKLRL	YSWFFFDVLI	KSMAQHLEIN	SKVKLLRNQR	FPASYHHAAE	TVVNLMPHI	TQKFGDNPEA 160
161	SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNHEHY	IPLNLPMPFG	KGRIQRYQDL 240
241	QLDYSLTDEF	CRNHFLVGLL	LREVGTAQOE	FREVRLIAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ 320
321	RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPQKGSTL	DNSLHKDLLG	AISGIASPYT	TSTPNINSVR	NADSRGSLIS 400
401	TDSGNLSPER	NSEKNSLSDK	HQOSSTLGNS	VVRCDKLDQS	EIKSLLMCFL	YILKSMSDDA	LFTYWNKAST	SELMOFFTTIS 480
481	EVCLHQFYM	GKRYIARNQE	GLGPVHDKR	SQTLFVSRNR	TGMMHARLQQ	LGSLDNSLTF	NHSYGHSDAD	VLHQSLLEAN 560
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVEDV	YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC 640
641	AALCYEILKC	CNSKLSSTRT	EASQLLYFLM	RNNFDYTGKK	SEVTRHLQVI	ISVSQLIADV	VGIGETRFQQ	SLSIINNCAN 720
721	SDRLIKHTSF	SSDVKDLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLDSMARIH	VKNGDLSEAA 800
801	MCYVHVHTALV	AEYLTRKGVF	RQGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY 880
881	KLIPIYIEKR	RDFEDEDGK	EYIYKEPKLT	PLSEISQRLI	KLYSDKFGSE	NVKMIQDSGK	VNPKDLDISKY	AXIQVTHVIP 960
961	FFDEKELQER	KTEFERSHNI	RREMFEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFPYVKK	RIPVMYQHHT	DLNPIEVAID 1040
1041	EMSKKVAELR	QLCSSAEVDM	IKLQKLQGS	VSVQVNAGPL	AYARAFDDT	NTKRYPDNKV	KLLKEVFRQF	VEACQCALAV 1120
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPT	STMVHGMTSS	SSVV 1195

FIG. 10E (cont.)

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	CCCCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC 80
81	GAATTCGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	TTTATGATG	AGATTAAAAAT	AGAGTTGCC	ACTCAGCTGC 160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCAGGAA	GAAGAGGGAT 240
241	GTCGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCCCTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCCAGC	AGCACATCCC 320
321	GGTCTCGGCG	AACCTTCCCT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAAT 400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTACATA 480
481	ATTTTTTCCA	GTACTGTGAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACTTG	TAAAGTACCT	TAAGAGTCTG 560
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTT	CGAGTCTCTA	CCAGAGCCAC 640
641	ACAGGAAGAA	GTGCGGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC 720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG 800
801	ACCAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCCTCACCCAG	CAACAAACTA	CTAGGTTACT	CATGGTTTTT 880
881	CTTTGATGTA	CTGATCAAAAT	CTATGGCTCA	GCATTTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTC 960
961	CTGCATCCTA	TCATCATGCA	CGGGAACCG	TTGTAAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA 1040
1041	GAGGCATCTA	AGAACCGGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCTTTGTCTT 1120
1121	CAAGCAGATC	AACAACTACA	TTAGCTGTTT	TGCTCCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC 1200
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACCT	ACCAATGCCA	TTTGAAAAG	CGAGGATTC	AAGTAACTCA 1280
1281	GACCTCCAGC	TTGACTACTC	AGGAGTTCC	TCTGATCGCC	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG 1360
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG 1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCCCTCTAC	CTGCCCTCTG	TGGTCTGCT	GATTGAAAAC 1520
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACCGCGG	CATGACCCGT	AAGGATGAAT	CCCTGGCTCT 1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAAGC	ACCCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA 1680
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTGAG	AGGATCTCTC 1760
1761	ATAAGCACAG	ATTCGGGTAA	CAGCCTTCCA	GAAAGGAATA	GTGAGAAAG	CAATCCCTG	GATAAGCACC	AACAAAGTAG 1840
1841	CACATTGGGA	AATTCGGTGG	TTGCTGTGTA	TAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA 1920
1921	TCTTAAAGAG	CATGCTGTAT	GATGCTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACCTTAAGA	ACCAGCTCCT 2000
2001	AGTTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT 2080
2081	AGTTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG 2160
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAAAC	ACAGCTATTG	CCACTCCGAG	GCAGATGTTT	TGCACCACTG	ATTACTTGAA 2240
2241	GCCAAACATTG	CTACTGAGGT	TTGCCGTGACA	GCTCTGGACA	CGCTTTCTCT	ATTTACATTG	CGCTTTAAGA	ACCAGCTCCT 2320
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGTCTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA 2400
2401	CGGCTTTAAA	AAATGTCTTC	ACTGCCCTTAA	GGTCCCTTAA	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC 2480
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGCTGTA	ACTCCAAAGT	GAGCTCCATC	AGGACGGAGG	CCTCCCAGCT 2560
2561	GCTCTACTTC	CTGATGAGGA	ACAACCTTGA	TTACACTGGA	AAGAAGTCTT	TGTCCGGGAC	ACATTTGCAA	GTCTCATAT 2640
2641	CTGTACAGCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGGA	AACGAGATT	CAGCAGTCCC	TGTCCATCAT	CAACAACGT 2720
2721	GCCAAACAGT	ACCGGCTTAT	TAAAGCACAC	AGCTTCTCT	CTGATGTGAA	GGACTTAAAC	AAAAGGATAC	GCACGGTGCT 2800
2801	AATGGCCACC	GCCCAGATGA	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT 2880
2881	ATGCCAGCAC	GCCCAGGCTC	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG 2960
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CAGCTCGAGT	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTACAA 3040
3041	CGCCTTCCAG	GTCATTACCC	CAAAATCGA	CGAGGAGGCC	TCCATGATGG	AAGACGTGGG	GATGCAAGAT	GTCCATTTC 3120
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGGCGAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC 3200
3201	ATCTACAAAC	TTATCATCCC	CATTATGAG	AAGCGGAGG	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTACAA 3280
3281	GGAAACCCAAA	CTCACACCCG	TGTCGGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAAATG 3360
3361	TCAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	TCTGGATTCT	AAGTATGCA	ACATCCAGGT	GACTCAGCTC 3440
3441	ATCCCTTCTT	TTGACGAAAA	AGAGTTGCAA	GAAAGGAAAA	CAGAGTTTGA	GAGATCCCA	AACATCCGCC	GCTTCATGTT 3520
3521	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGGCGGG	GTGGAAGAGC	AGTGCAAAAC	GCGCACCATC	CTGACAGCCA 3600
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCTGTGAT	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC 3680
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT 3760
3761	CAAACTCCAG	GGCAGCGTGA	GTGTTTCAAGT	CAATGCTGGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA 3840
3841	CAAAGCGATA	TCCTGACAAT	AAAGTGAAGC	TGCTTAAAGA	AGTTTTCAGG	CAATTTGTGG	AAGCTTGCGG	TCAAGCCTTA 3920
3921	GCGGTAACG	AACGTCTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG	AAATGGCGAA 4000
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT 4080
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTGCTGTG	ATTACATCTC 4160
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACT	CAGGATGCTT	TCCAAAGCCT	ATCACTGGGG	AGACCGAGCA 4240
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA 4320
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAAGTTTTC	ATTGTGTCTT	AACAAAGGTG	TGGTAGACAC 4400
4401	TCTTGAGCTG	GACTTAGATT	TTATCTTCTC	TTGACAGATA	TGTGTTAGAT	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG 4480
4481	ATCTACATGG	CAGGAGGGGC	TGCACTGACA	TTGATGCCCTG	GGGACCTT	TGCTCGACT	CGTGCCGGAA	ATCTGATCGT 4560
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTTGTC	TAGGAGTATG	TTGTATGACT	AGGATTGTTG	CTATTATCTC	ATCAACAAC 4640
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TAAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCAATTA 4720
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTCTTA	CATTTTTAAT	ACTCACATGG	GCTTATGCAT	TAAGTTTAAAT 4800
4801	TGTATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTGTGTCAT	AAAAATGTGC	AATATGGAGA 4880
4881	TGTATAAAG	TCTTTACT						4898

FIG.10F

		10		20		30		40			50		60		70		80	
1	MEGHVMIAFL	PTILNQLFRV	LTRATQEEVA	VNVTRVIIHV	VAQCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK	80									
81	SMTTILKPSA	DELTSENKLLR	YSWFFFDVLI	KSMAQH LIEN	SKVKLLRNQR	FPASYHHAAE	TVVNMLMPHI	TQKFGDNPEA	160									
161	SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLEFYKFEF	LRVVCNHEHY	IPINLPMPPG	KGRIQRYQDL	240									
241	QLDYSLTDEF	CRNHFLVGLL	LREVG TALQE	FREVRLIAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ	320									
321	RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPOKGSTL	DNSLHKDILG	AISG IASPYT	TSTPNINSVR	NADSRGSLIS	400									
401	TDSGNSLPER	NSEKSNSLDK	HQOSSTLGNS	VVRCDKLDQS	EIKSLIMCFL	YILKSMSDDA	LFTYWNKAST	SELMDFFTIS	480									
481	EVCLHQFQYM	GKRYIARNQE	GLGPIVHDRK	SQTLFVSRNR	TGMMHARLQQ	LGSLDNSLTF	NHSYGHSDAD	VLHQSLLEAN	560									
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVFTA	LRS LIYKFPS	TFYEGRADMC	640									
641	AALCYEILKC	CNSKLSSIRT	EASQLLYFILM	RNNFDYTGKK	SFVRTHLQVI	ISVSQ LIADV	VGIGETRFQQ	SLSIINN CAN	720									
721	SDRLIKHTSF	SSDVKDLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLD SMARIH	VKNGDLSEAA	800									
801	MCYVHV TALV	AEYLTRKGVF	RQGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY	880									
881	KLIIP IYEKR	RDFFEDEDGK	EYIYKEPKLT	PLSEISQRLI	KLYSDKFGSE	NVKMIQDSGK	VNPKOLD SKY	AYIQVTHVIP	960									
961	FFDEKELQER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFPPYVKK	RIPVMYQHHT	DLNPIEVAID	1040									
1041	EMSKKVAELR	QLCSSAEVDM	IKLQKLQGS	VSVQVNAGPL	AYARAF LDDT	NTKRYPDNKV	KLLKEVFRQF	VEACGQALAV	1120									
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLENSLH	IFNAISGTPT	STMVHGMTSS	SSVV	1195									
		10		20		30		40			50		60		70		80	

FIG. 10F (cont.)

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCTC	GAGGTGACG	GTATCGATAA	GCTTGATATC 80
81	GAATTTCGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	TTTATGATG	AGATTAATAA	AGAGTTGCC	ACTCAGCTGC 160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCAG	CTGTGACAA	TCAAGTAAAG	GAAGCAGCAA	GAAGAGGGAT 240
241	GTCGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCTCC	TGAAAGACGG	AAGGTTGGTG	ACAAGCGAGC	AGCACATCCC 320
321	GGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAT 400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTACATA 480
481	ATTTTTCCTA	GTACTGTGAG	AAAACCGAAT	CTGGAGCCCC	AGCCTTAGGA	AACGAACTTG	TAAAGTACCT	TAAGAGTCTG 560
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTT	CGAGTCCCTA	CCAGAGCCAC 640
641	ACAGGAAGAA	GTCGCGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC 720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG 800
801	ACCAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCCTCAACAG	CAACAACTA	CTGAGGTACT	CATGGTTTTT 880
881	CTTTGATGTA	CTGATCAAAT	CTATGGCTCA	GCATTTGATA	GAGAATCCA	AAGTTAAGTT	GCTGCCAAAC	CAGAGATTTT 960
961	CTGCATCCTA	TCATCATGCA	GCGGAAACCG	TTGTAAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA 1040
1041	GAGGCATCTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTACCTTTC	ATGGACAGGG	GCTTTGTCTT 1120
1121	CAAGCAGATC	AACAACATCA	TTAGCTGTTT	TGCTCCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC 1200
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACCT	ACCAATGCCA	TTTGGAAAAA	GCAGGATTCA	AAGATACCAA 1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GAACCAACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG 1360
1361	GACGACCTTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG 1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTTAC	CTGCTCTGT	TTGGTCTGCT	GATTGAAAAA 1520
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCTGGCTCT 1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAAGC	ACCCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGCGGCCA 1680
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTGCG	AGGATCTCTC 1760
1761	ATAAGCAGAG	ATTCGGGTAA	CAGCCTTCCA	GAAGGAATA	GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG 1840
1841	CACATTGGGA	AATTCGCTGG	TTGCTGTGTA	TAAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA 1920
1921	TCTTAAAGAG	CATGTCTGAT	GATGCTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACCTTATGA	TTTTTTTACA 2000
2001	ATATCTGAAG	TCTGCCTGCA	CCAGTTCCAG	TACATGGGGA	AGCAGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT 2080
2081	AGTTACATGT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	ACAGAAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG 2160
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAAAC	ACAGCTATGG	CCACTCGGAC	GCAGATGTTT	TGCACAGATC	ATTACTTGAA 2240
2241	GCCAAATATG	CTACTGAGGT	TTGCCTGACA	GCTCTGGACA	CGCTTTTCTT	ATTTACATTG	CGGTTTAAAG	ACCAGTCTCT 2320
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGTCTTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA 2400
2401	CGGCTTTAAA	AAATGTCTTC	ACTGCCTTAA	GGTCTTAAAT	TTATAAGTTT	CCCTCAACAT	TCTATGAAG	GAGAGCGGAC 2480
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGTCTGA	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCAGCT 2560
2561	GCTCTACTTC	CTGATGAGGA	ACAACTTTGA	TTACACTTGA	AAGAAGTCTT	TTGTCCGGAC	ACATTTGCAA	GTCATCATAT 2640
2641	CTGTACGCCA	GCTGATAGCA	GACGTGTTG	GCATTGGGGA	ACACAGATTC	CAGCAGTCCC	TGTCCATCAT	CAACAACCTG 2720
2721	GCCAAACAGT	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT	CTGATGTGAA	GGACTTAAAC	AAAGGATAC	GCACGGTGCT 2800
2801	AATGGCCACC	GCCAGATGA	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT 2880
2881	ATGCCAGCAC	GCCGAGCTC	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG 2960
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AATATCTCAC	ACGGAAGGCG	GTGTTTAGAC	AAGGATGCAC 3040
3041	CGCCTTCAGG	GTCATTACCC	CAAAACATCGA	CGAGGAGGCC	TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTTC 3120
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGGCAGGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC 3200
3201	ATCTACAAAC	TTATCATCCC	CATTTATGAG	AAGCGGAGGG	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTTCAA 3280
3281	GGAAACCCAA	CTCACACCCG	TGTCGGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAAATG 3360
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCTAAGGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCACGCT 3440
3441	ATCCCTTCTT	TTGACGAAAA	AGAGTTGCAA	GAAGGAAAAA	CAGAGTTTGA	GAGATCCAC	AACATCCGCC	GCTTCATGTT 3520
3521	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGCGGGG	GTGGAAGAGC	AGTGCAAACG	GCGCACCATC	CTGACAGCCA 3600
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCTAT	TGACCAAGAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC 3680
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	GTGCTCTCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT 3760
3761	CAAACTCCAG	GGCAGCGTGA	GTGTTCAAGT	CAATGCTGGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA 3840
3841	CAAAGCGATA	TCCTGACAA	AAAGTGAAGC	TGCTTAAAGGA	AGTTTTTCAGG	CAATTTGTGG	AAGCTTGGCG	TCAAGCCTTA 3920
3921	GCGGTAAACG	AACGTCTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACCTACAGG	AAATGGCGAA 4000
4001	GGAGCTTTCT	GAATCATGTC	ATGAGCAGAT	CTGCCCCCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT 4080
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGTCTGTTG	ATTACATCTC 4160
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA 4240
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA 4320
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAGATTTTC	ATTGTTGCTT	AACAAAGGTG	TGGTAGACAC 4400
4401	TCTTGAGCTG	GACTTAGATT	TTATTCTTCC	TTGCAGAGTA	GTGTTAGAA	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG 4480
4481	ATCTCATGAG	CAGGAGGGGC	TGCAGTGACA	TTGATGCTGT	GGGGACCTTT	TGCCTCGACT	CGTGCCGGAA	ATCTGATCGT 4560
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTTGTC	TAGGAGTATG	TTGTATGACT	AGGATTGTGT	CTATATATCT	ATTCAACAAC 4640
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCATTAA 4720
4721	TCATCGACTC	CGGACCGGTC	ATATATGTAT	TACATTTCTA	CATTTTTAAT	ACTCACATGG	GCTTATGCAT	TAAGTTTAAAT 4800
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTTGTCTAT	AAAAATGTGC	AATATGGAGA 4880
4881	TGTATACAAG	TCTTTACT						4898

FIG.10G

	10	20	30	40	50	60	70	80
1	MEGHVMI AFL	PTILNQLFRV	LTRATQEEVA	VNVTRV I I HV	VAQCHEEGLE	SHLSYV KYA	YKAEPY VASE	YKTVHEELTK 80
81	SMTILKPSA	DFLT SNKLLR	YSWFFFDVLI	KSMAQH LIEN	SKVKLLRNQR	FPASYH HAAE	TVVNMLMPHI	TQKF GDNPEA 160
161	SKNANHSLAV	FIKRCET FMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNHEHY	IPLNLPM PFG	KGRIQRYQDL 240
241	QLDYSLTDEF	CRNHFLVGLL	LREVG TALQE	FREVRLIAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ 320
321	RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPQKGSTL	DNSLHKDLLG	AISGIASPYT	TSTPNINSVR	NADSRGSLIS 400
401	TDSGNSLPER	NSEKSNSLDK	HQQSSTLGNS	VVRCDKLDQS	EIKSLLMCFI	YILKMSDDA	LEFTYWNKAST	SEIMDEFTIS 480
481	EVCLHQFQYM	GKRYIARNQE	GLGPIVHDRK	SQTLFVSRNR	TGMMHARLQQ	LGSLDNLSTF	NHSYGHSDAD	VLHQSLLEAN 560
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC 640
641	AALCYEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGKK	SEVTRTHLQVI	ISVSQLIADV	VGIGETRFQQ	SLSIINN CAN 720
721	SDRLIKHTSF	SSDVKDLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLD SMARIH	VKNGDLSEAA 800
801	MCYVHV TALV	AEYLTRKGVF	RQGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY 880
881	KLIIP IYEKR	RDFFEDEDGK	EYIYKEPKLT	PLSEISQRLL	KLYSDKFGSE	NVKMIQDSGK	VNPKDLDSKY	AYIQVTHVIP 960
961	FFDEKEIQER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFPYVKK	RIPVMYQHHT	DINPIEVAID 1040
1041	EMSKKVAELR	QLCSSAEVDM	IKLQLKLQGS	VSVQVNAGPL	AYARAF LDDT	NTKRYPDNKV	KLLKEVFRQF	VEACGQALAV 1120
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPT	STMVHGMTSS	SSVV 1195

FIG. 10G (cont.)

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GGGGGGGCTC	GAGGTGACG	GTATCGATAA	GCTTGATATC 80
81	GAATTCGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAAA	AGAGTTGCCC	ACTCAGCTGC 160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCACGAA	GAAGAGGGAT 240
241	GTCGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCTTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC 320
321	GGTCTCGGCG	AACCTTCCCT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAT 400
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTACATA 480
481	ATTTTTTCCA	GTACTGTCAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACTTG	TAAAGTACCT	TAAGAGTCGG 560
561	CATGCCATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTT	CGAGTCTCTA	CCAGAGCCAC 640
641	ACAGGAAGAA	GTGCGGGTAA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC 720
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG 800
801	ACCAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTC 960
881	CTTTGATGTA	CTGATCAAAAT	CTATGGCTCA	GCATTTGATA	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	CAGATATCCA 1040
961	CTGCATCCTA	TCATCATGCA	CGCGAAACCG	TTGTAAATAT	TCCTCACCAG	CAACAAACTA	CTGAGGTACT	CATGGTTTTT 880
1041	GAGGCATCTA	AGAAGCGGAA	TCATAGCCTT	GCTTGCTTCA	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTC 960
1121	CAAGCAGATC	AACAACCTACA	TTAGCTGTTT	TGCTCCTGGA	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	CAGATATCCA 1040
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACTT	TCAAGAGATG	TTTCACTTTC	ATGGACAGGG	GCTTTGTCTT 1120
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTCTCTCA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC 1200
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCGG	TCTGATCGCC	ACCAATGCCA	TTTGGAAAAG	CGAGGATTCA	AAGATACCAA 1280
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	GAACACCACT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG 1360
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCCT	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG 1440
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAAGC	CACCCCTCTAC	CTGCCCTCTG	TTGGTCTGCT	GATTGAAAAC 1520
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	TGAACCGGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT 1600
1761	ATAAGCACAG	ATTCCGGTAA	CAGCCTTCCA	GAAGGGAATA	ACCCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA 1680
1841	CACATTGGGA	AATTCGGTGG	TTCCGCTGTA	TAACTTGAC	CATCAACAGT	GTGAGAAATG	CTGATTCCAG	AGGATCTCTC 1760
1921	TCTTAAAGAG	CATGCTGAT	GATGCTTTGT	TTACATATTG	GTGAGAAGAG	CAATTCCTTG	GATAAGCACC	AACAAAGTAG 1840
2001	ATATCTCAGC	TTGACTTCCA	CCAGTTCAGG	TACATGGGGA	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA 1920
2081	AGTTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	GAACAAGGCT	TCAACATCTG	AACCTTATGA	TTTTTTTACA 2000
2161	GCAGCTTGGA	TCTACTCTCT	ACTTTTAAAC	ACAGCTATGG	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT 2080
2241	GCCAACTATG	CTACTGAGGT	TTGCCGTGAC	GCTCTGGACA	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG 2160
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	CCACTCGGAC	GCAGATGTTT	TGCACCACTG	ATTACTTGAA 2240
2401	CGGCTTTAAA	AAATGTCTTC	ACTGCCCTTA	GGTCTTAAAT	CGGTTTCTCT	ATTTACATTG	GGCTTTAAGA	ACCAGCTCCT 2320
2481	ATGTGTGCGG	CTGTGTGTTA	CGAGATTCTC	AAGTGCCTGA	GATGTCTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA 2400
2561	GCTCTACTTC	CTGATGAGGA	ACAACCTTGA	TTACACATGA	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGACCGGAC 2480
2641	CTGTACAGCA	GCTGATAGCA	GACGTGTTG	GCATTGGGGA	ATCCAGATTG	CAGCAGTCCC	TGCTCCATAT	CAACACATGT 2560
2721	GCCAAACAGT	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT	CTGATGTGAA	GGACTTAAAC	AAAAGGATAC	GCACGGTGCT 2640
2801	AATGGGCCACC	GCCAGATGTA	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT 2720
2881	ATGCCAGCAG	CGCCGAGCTC	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG 2800
2961	CGCCTTCAGG	GTCATTACCC	CAACATCGA	CGAGGAGGCC	AATATCTCAC	ACGGAAGGCG	GTGTTTAGAC	AAGGATGCAC 2880
3041	GCAGCTGAGT	GCTGATGGAG	CTCCTTGAGC	AGTGCGCAGA	TCCATGATGG	AAGACGTGGG	GATGCAAGGT	GTCCATTTCAT 2960
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCGCAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC 3040
3201	ATCTACAAAC	TTATCATCCC	CATTATGAG	AAGCGGAGGG	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTTACA 3120
3281	GGAAACCCAAA	CTCACACCCG	TGTCGGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTAATCGGA	TAAATTTGGT	TCTGAAAATG 3200
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCACGTC 3280
3441	ATCCCTTTCT	TTGACGAAAA	AGAGTTGCAA	GAAGGAAAAA	CAGAGTTTGA	GAGATCCCAC	AACATCCGCC	GCTTCATGTT 3360
3521	TGAGATGCCA	TTTACGCGA	CCGGGAAGAG	GCAGGGCGGG	GTGGAAGAGC	AGTGCAAAAC	CGCGACCATC	CTGACAGCCA 3440
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCTAT	GTGCTCCCTC	GGCCGAGGTG	GACATGATCA	AACATGCAGT 3520
3681	ATTTGACGAG	TGAGTAAGAA	GGTGGCGGAG	CTCCGCGCAG	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAAAC 3600
3761	CAAACCTCCAG	GGCAGCGTGA	GTGTTCCAGT	CAATGCTGGC	AGTTTTCAGG	CAATTGTGCG	AAGCTTGGCG	TCAAGCCTTA 3680
3841	CAAAGCGGATA	TCCTGACAAT	AAAGTGAAGC	TGCTTAAAGGA	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG	AAATGGCGAA 3760
3921	GGAGCTTTCT	GAATCATGTC	ATGAGCAGAT	CTGCCCCCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCG	CTTCACATCT 3840
4001	TCAAACTGCT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTCTGTGT	ATTACATCTC 3920
4081	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAAAT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA 4000
4161	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA 4080
4241	AGAAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAAGTTTTT	ATTGTGTCTT	AACAAGGTG	TGGTAGACAC 4160
4321	TCTTGAGCTG	GACTTAGATT	TTATTCTTCC	TTGCAGAGTA	GGGAGACCTT	TGCCTCGACT	CGTGCCGGAA	ATCTGATCGT 4240
4401	ATCTACATGG	CAGGGAGGGC	TGCATGACA	TTGATGCTGT	TTGTATGACT	AGGATTTGTG	CTATTATCTC	ATTCAACAAC 4320
4481	AATCAGGGTA	CAGAACCTTAC	TAGTTTTGTC	TAGGAGTATG	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCAATTAA 4400
4561	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	CATTTTTTAA	ACTCACATGG	GCTTATGCAT	TAAGTTTAAAT 4480
4641	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA	TAATGGTTTA	TTCTTGTCAT	AAAAATGTGC	AATATGGAGA 4560
4721	TGTGATAAAT	TTTGCTGTGT	CCAGTATATG	CAATACACTT				4880
4801	TGTATACAAG	TCTTTACT						4898
4881								

FIG.10H

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		10		20		30		40			50		60		70		80	
1	MEGHV	MIAFL	PTIIN	QLFRV	LTRAT	QEEVA	VNVTR	VIIHV	VAQC	CHEEGLE	SHLSY	VKYA	YKAEP	YVASE	YKTV	HEELTK	80	
81	SMTTIL	KPSA	DELT	SNKLLR	YSWFF	FDVLI	KSMAQ	HLIEN	SKVK	LLRNQR	FPASY	HHAEE	TVVN	NMLPHI	TQKF	GDNPEA	160	
161	SKNANH	SLAV	FIKRC	FTFMD	RCFV	FKQINN	YISCF	APGDP	KTLE	FEYKFEF	LRVVC	NHEHY	IPLNL	PMPFG	KGRI	QRYQDL	240	
241	QLDYSL	TDEF	CRNH	FLVGLL	LREVG	TALQE	FREV	LLIAIS	VLQN	LLIKHS	FDDRY	ASRSH	QARI	ATLYLP	LFGL	LIENVQ	320	
321	RINVR	DVSPF	PVNAG	MTVKD	ESLAL	PAVNP	LVTP	QKGSTL	DNSL	HKDLLG	AISGI	ASPYT	TSTPN	INSVR	NADSR	GSGLIS	400	
401	TDSGN	SLPER	NSEKS	NSLDK	HQQS	SSTLGS	VVRCD	KLDQS	EIKS	LLMCFL	YILKS	MSDDA	LFTY	WNKAST	SELM	DFFTTIS	480	
481	EVCLH	QFQYM	GKRYI	ARNQE	GLGPI	VHDRK	SQTL	PVSRNR	TGMH	ARLQQ	LGSL	DNSLTF	NHSY	GHSAD	VLHQ	SLLLEAN	560	
561	IATEV	CLTAL	DTLS	SLFTLAF	KNQL	LADHGH	NPLMK	KVFDV	YLCF	LQKHQS	ETALK	NVFTA	LRSL	IYKFPS	TFYE	GRADMC	640	
641	AALCY	EILKC	CNSKL	SSIRT	EASQL	LYFLM	RNNFD	YTGKK	SEVR	THLQVI	ISVS	QLIADV	VGIG	ETREFQ	SLSI	INNCAN	720	
721	SDRLI	KHTSF	SSDV	KDLTKR	IRTV	LMATAQ	MKEH	ENDPEM	LVDL	QYSLAK	SYAST	PELRK	TWLD	SMARIH	VKNG	DLSEAA	800	
801	MCYVH	VHTALV	AEYL	TRKGVF	RQGC	TAFRVI	TPNI	DEEASM	MEDV	GMDQDVH	FNED	VLMELL	EQCA	DGLWKA	ERYE	LIADIY	880	
881	KLIIP	IYEKR	RDFFE	DEDEGK	EYIY	KEPKLT	PLSE	ISQRL	KLYS	DKFGSE	NVKMI	QDSGK	VNPK	DLDISKY	AYIQ	VTHVIP	960	
961	FFDEK	ELQER	KTEFE	RSRSHNI	RRFM	FEMPFT	QTGK	RQGGVE	EQCK	RRTILT	AIHCF	PYVKK	RIPV	MYQHHT	DLNP	IEVAID	1040	
1041	EMSKK	VAELR	QLCSS	AEVDM	IKLQ	LKLQGS	VSVQ	VNAGPL	AYAR	AFLLDT	NTKRY	PDNKV	KLLK	EVFRQF	VEAC	GQALAV	1120	
1121	NERLI	KEDQL	EYQE	EMKANY	REMAK	ELSEI	MHEQ	ICPLEE	KTSL	VPNSLH	IFNA	ISGTPT	STMV	HGMTSS	SSVV		1195	
		10		20		30		40			50		60		70		80	

FIG. 10H (cont.)